FIG. 1

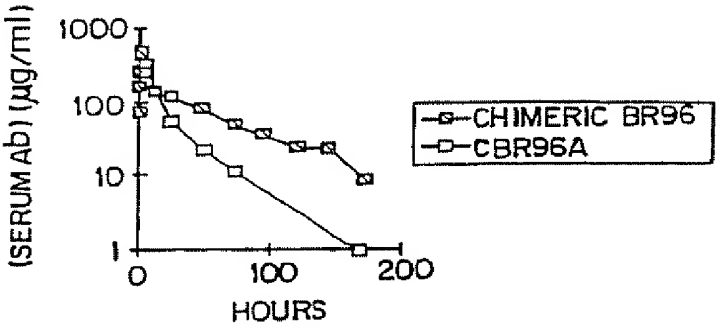

(SERUM Ab) (µg/ml)
1000
100
10
1
0
100
200
HOURS
CHIMERIC BR96
CBR96A

FIG. 2

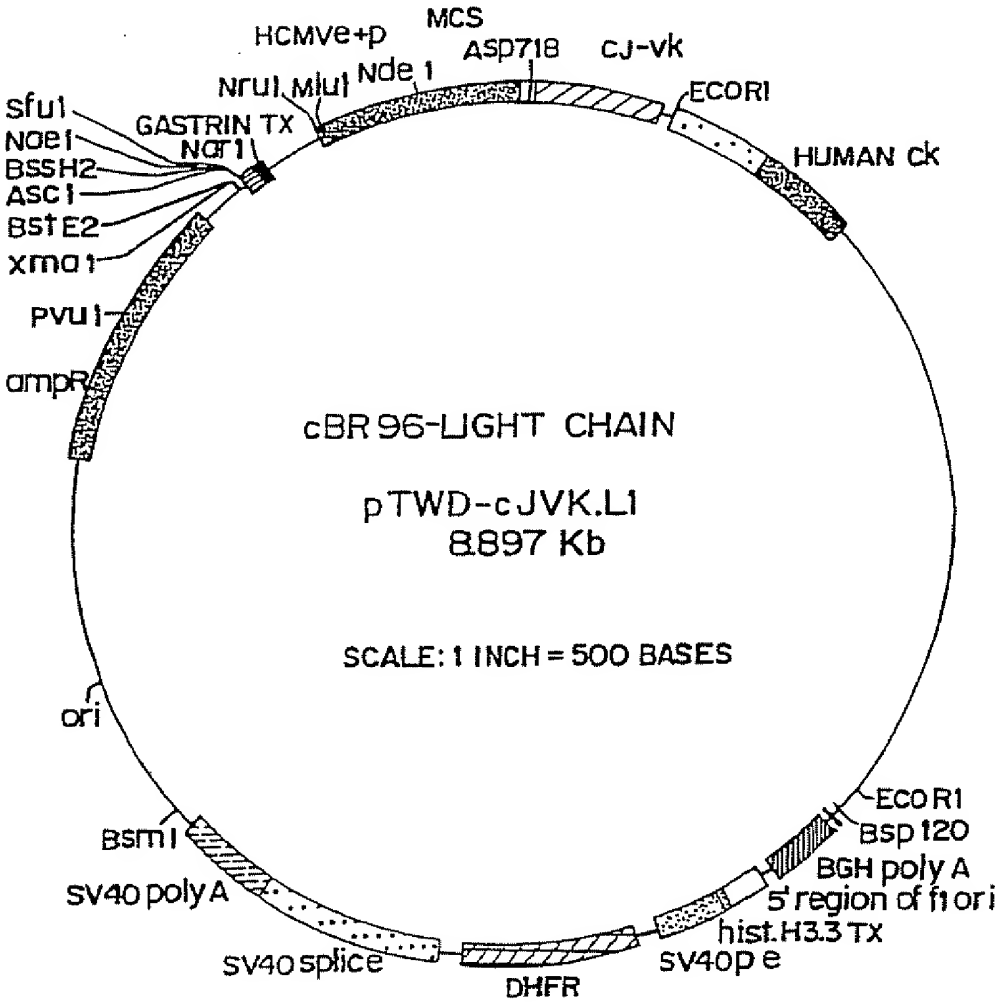

MCS
HCMVe+p
ASP718
CJ-vk
Nde 1
Nrul Mlul
ECORI
Sfu1
GASTRIN TX
NOe1
Nar1
BSSH2
ASC1
BSTE2
xma1
HUMAN Ck
PVU1
ampR
cBR96-LIGHT CHAIN
pTWD-cJVK.L1
8.897 Kb
SCALE: 1 INCH = 500 BASES
ori
ECO R1
Bsm1
Bsp 120
BGH poly A
SV40 poly A
5' region of f1 ori
hist.H3.3 TX
SV40 splice
SV40p e
DHFR

FIG. 3

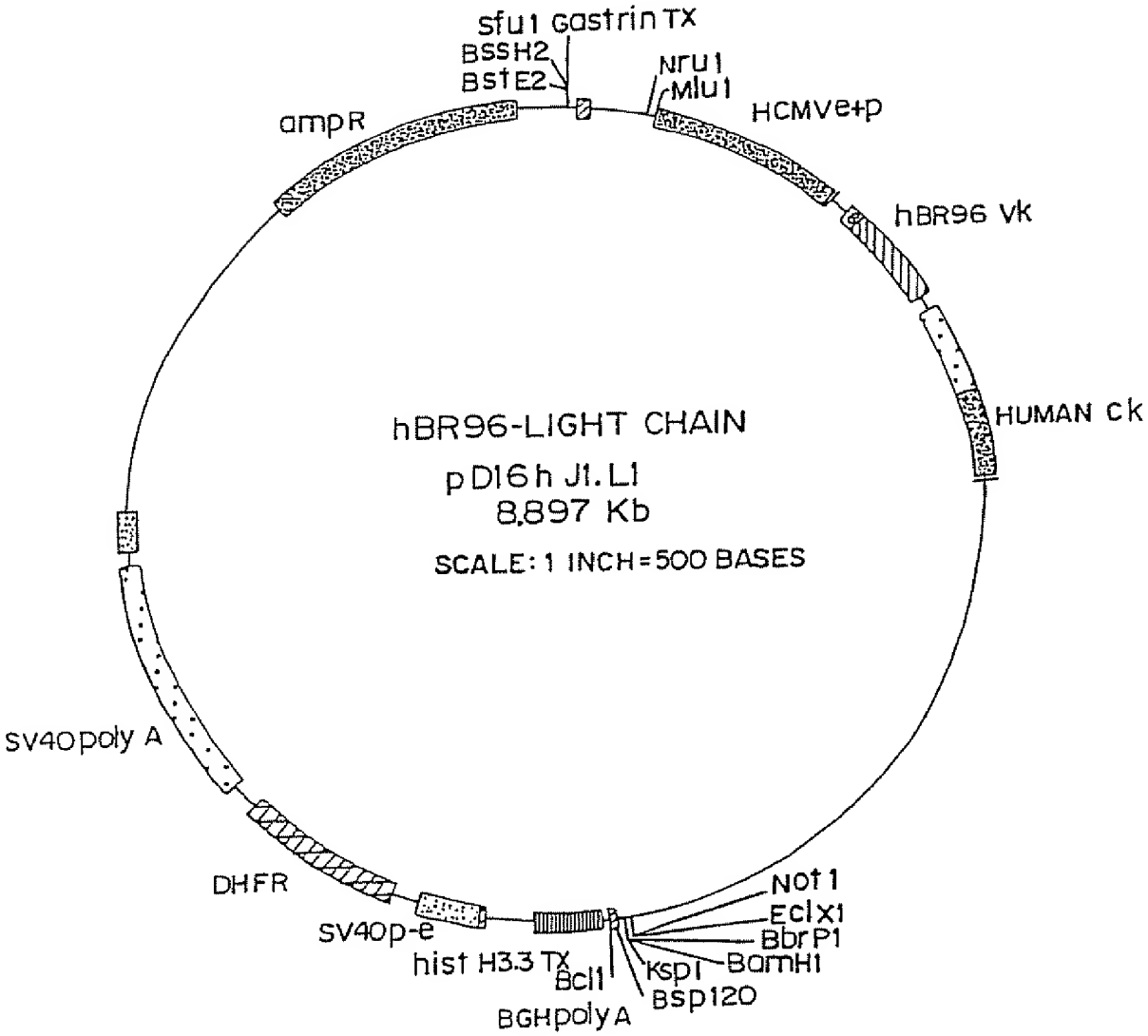

sfu1 Gastrin TX
BSSH2
BstE2
Nru1
Mlu1
HCMVe+p
ampR
hBR96 Vk
HUMAN ck
hBR96-LIGHT CHAIN
pD16h J1. L1
8.897 Kb
SCALE: 1 INCH = 500 BASES
sv40poly A
DHFR
sv40p-e
hist H3.3 TX
Bcl1
BGHpoly A
Not 1
EclX1
BbrP1
Kspl
BamH1
Bsp120

FIG. 4

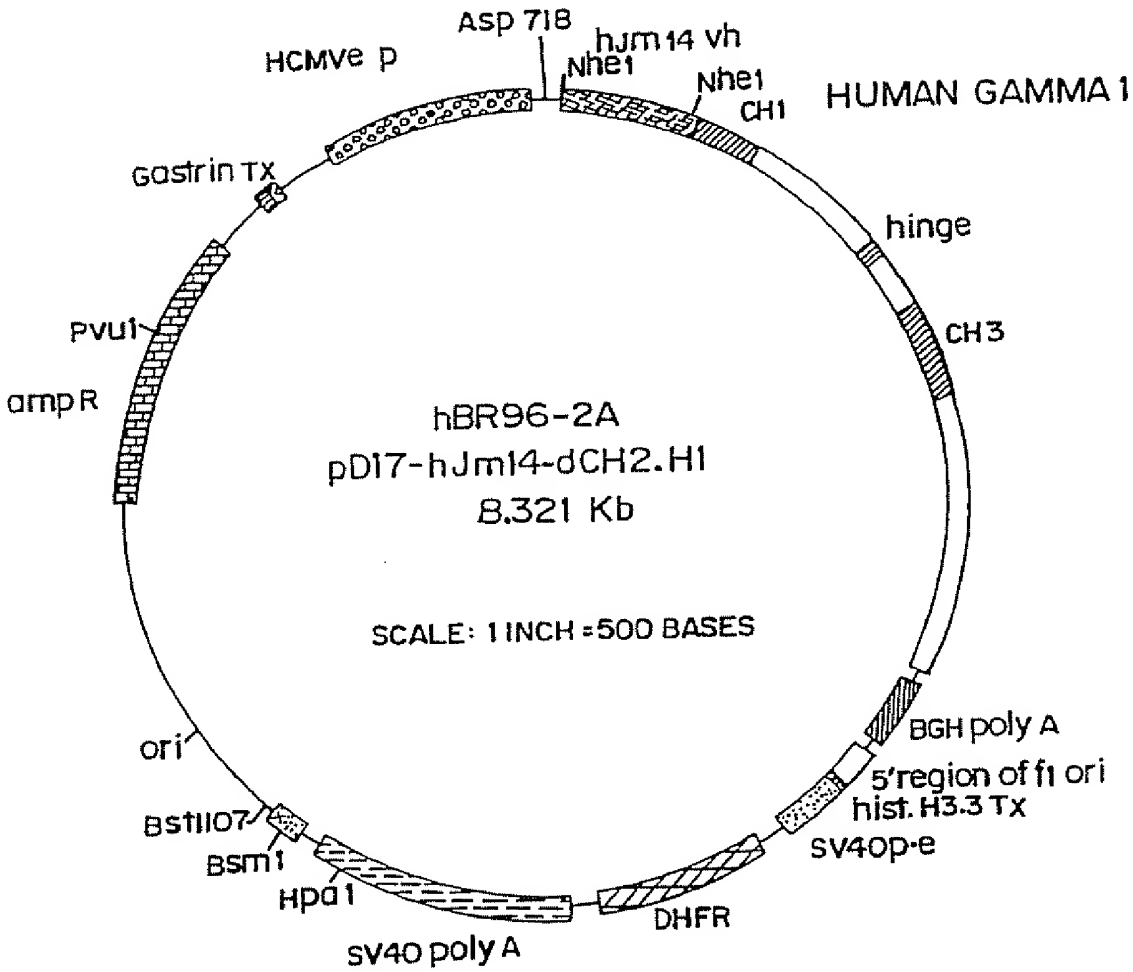

Asp 718
hJm14 vh
Nhe1
Nhe1
CH1
HUMAN GAMMA 1
HCMVe p
Gastrin TX
hinge
CH3
Pvu1
ampR
hBR96-2A
pD17-hJm14-dCH2.H1
8.321 Kb
SCALE: 1 INCH =500 BASES
BGH poly A
5'region of f1 ori
hist. H3.3 Tx
SV40p-e
ori
BstII07
Bsm1
Hpa1
DHFR
SV40 poly A

FIG. 5

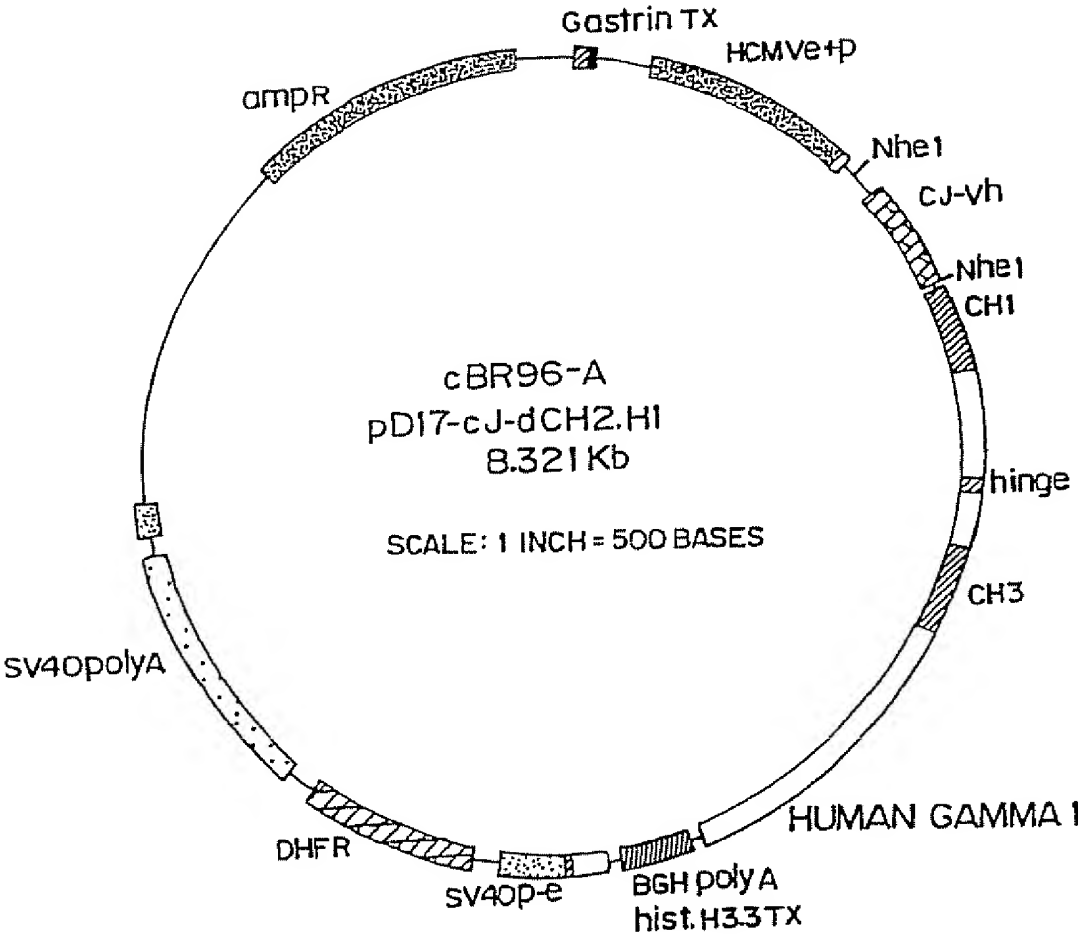

Gastrin TX
HCMVe+p
ampR
Nhe1
cJ-vh
Nhe1
CH1
cBR96-A
pD17-cJ-dCH2.H1
8.321 Kb
SCALE: 1 INCH = 500 BASES
hinge
CH3
SV40polyA
HUMAN GAMMA 1
DHFR
SV40p-e
BGH poly A
hist. H3.3TX

FIG. 6

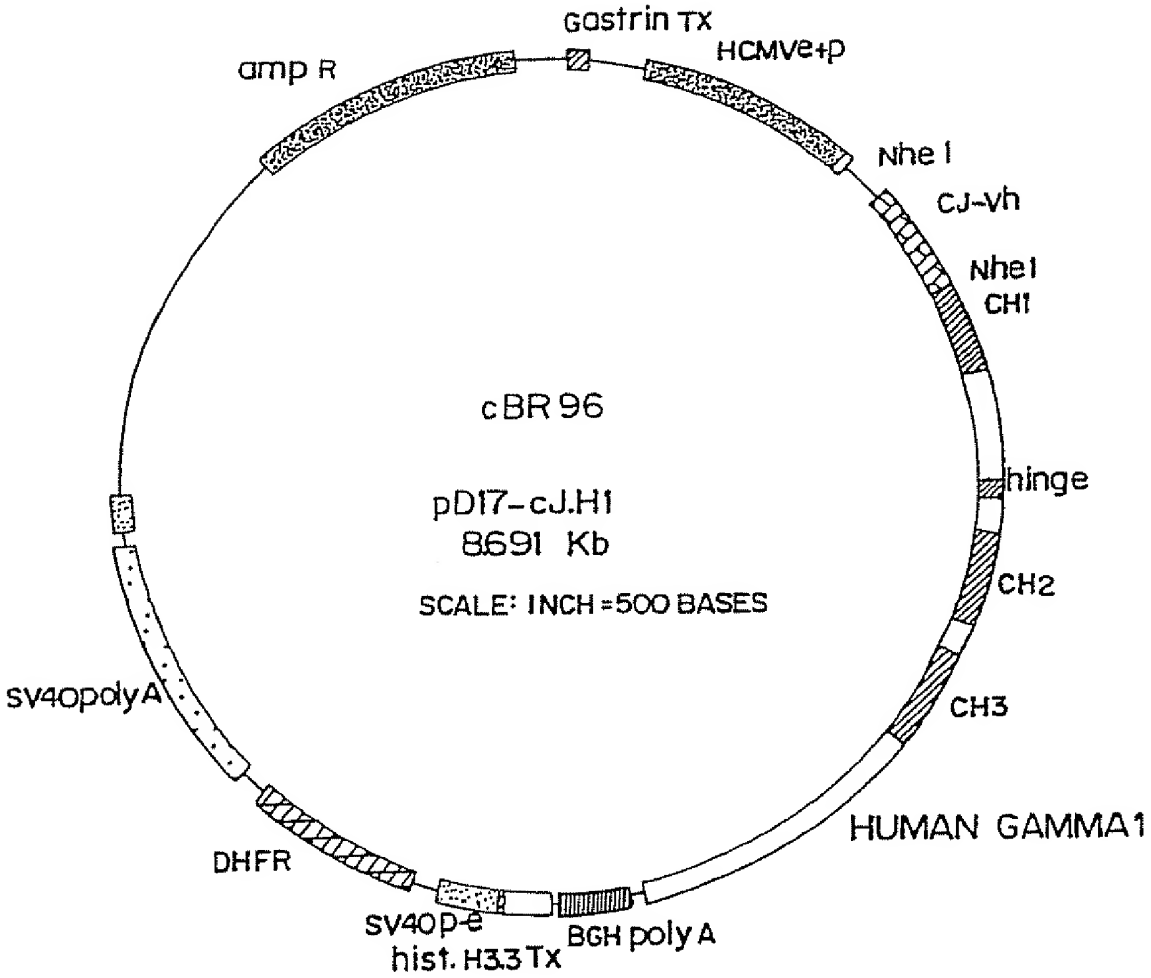

Gastrin TX
HCMVe+p
amp R
Nhe I
CJ-Vh
Nhe I
CH1
cBR 96
pD17-cJ.H1
8.691 Kb
SCALE: INCH =500 BASES
hinge
CH2
CH3
HUMAN GAMMA1
SV40polyA
DHFR
SV40p-e
hist. H3.3 Tx
BGH poly A

FIG. 7

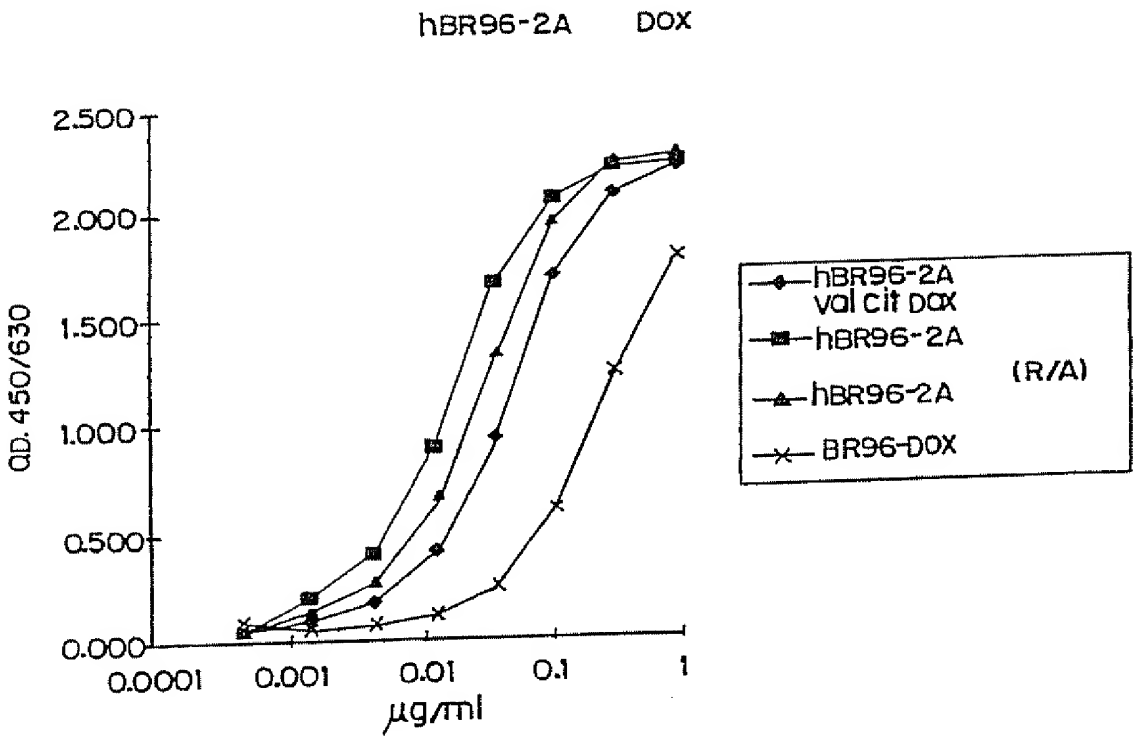

hBR96-2A DOX
2.500
2.000
1.500
1.000
0.500
0.000
O.D. 450/630
0.0001
0.001
0.01
0.1
1
μg/ml
hBR96-2A val cit DOX
hBR96-2A
hBR96-2A
BR96-DOX
(R/A)

FIG. 8

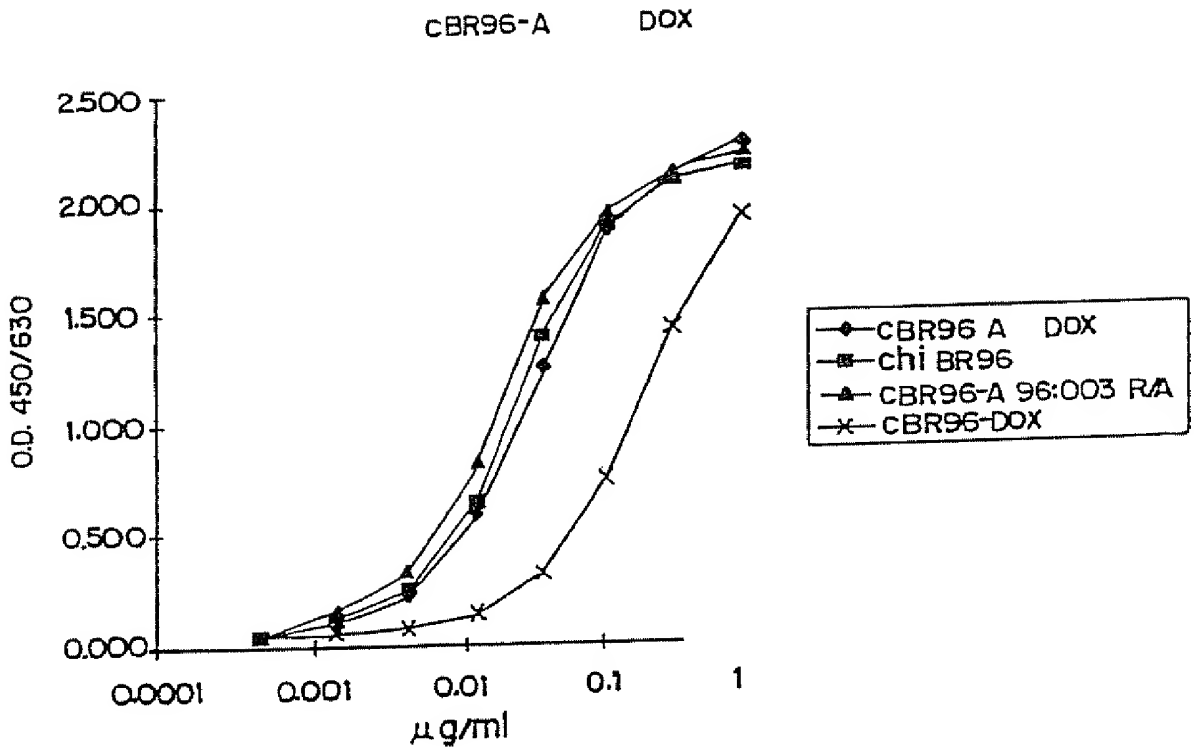

cBR96-A DOX
2.500
2.000
1.500
1.000
0.500
0.000
O.D. 450/630
0.0001
0.001
0.01
0.1
1
µg/ml
cBR96 A DOX
chi BR96
cBR96-A 96:003 R/A
cBR96-DOX

FIG. 9A

A-HINGE + CH2 + CH3 DOMAINS WERE REMOVED FROM BR96 IgG1 CONSTRUCT BY E.CO.47-III RESTRICTION DIGESTION.

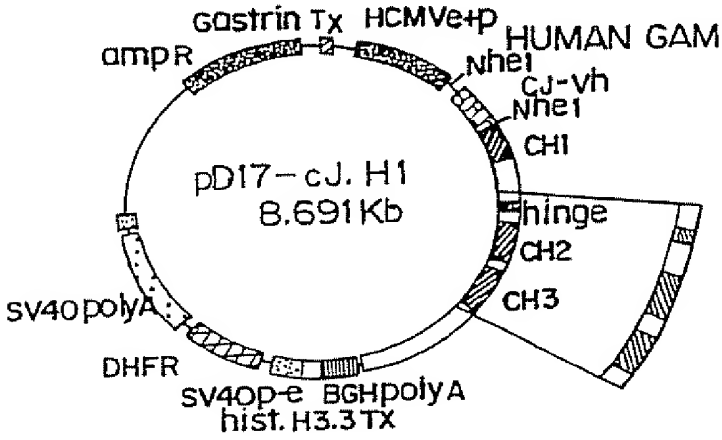


FIG. 9B

B-HINGE+CH3 DOMAINS AMPLIFIED BY PCR FROM L6 IgG1 CONSTRUCT LACKING THE CH2 DOMAIN.

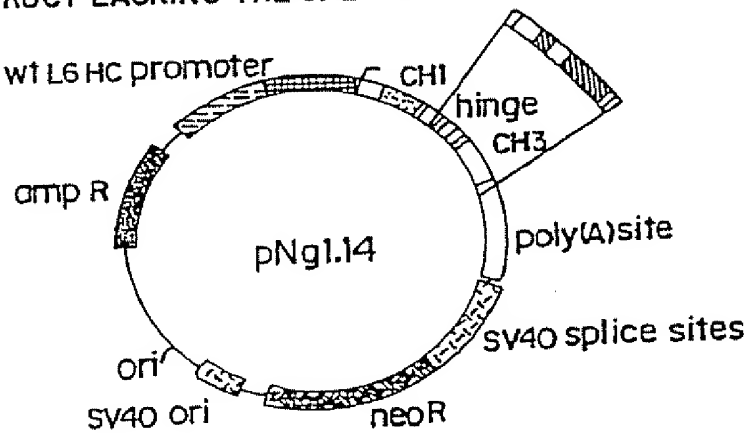
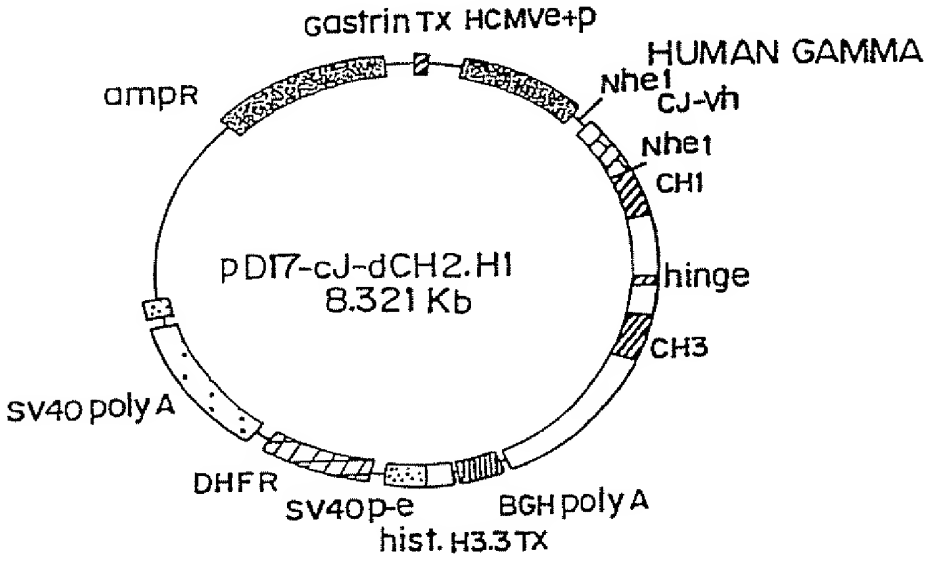


FIG. 9C

C-HINGE+CH3 PCR FRAGMENT CLONED BY HOMOLOGOUS RECOMBINATION INTO E.CO.47-III SITE OF BR96 IGG1 MOLECULE.



1.- INTRODUCTION OF MUTATIONS BY SITE DIRECTED MUTAGENESIS ON DOUBLE-STRANDED PLASMID DNA.

FIG. 10A

A.- MUTATIONS INTRODUCED INTO SYNTHETIC OLIGONUCLEOTIDES USED FOR THE PCR AMPLIFICATION OF CH2 DOMAIN

FIG. 10B

B.- PLASMID DNA LINEARIZED INSIDE CH2 DOMAIN AND CO-TRANSFORMED WITH PCR FRAGMENT INTO COMPETENT DH5α

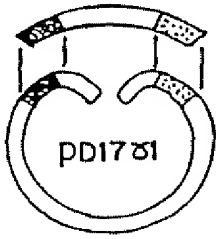


FIG. 10C

C.- CLONING MEDIATED BY HOMOLOGOUS RECOMBINATION YIELDS TRANSFORMANTS HARBOURING RECOMBINANT PLASMIDS.

FIG. 11

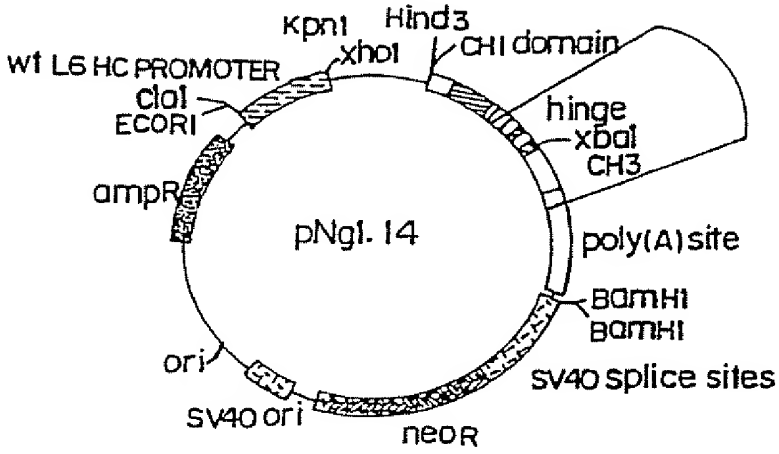


FIG. 12

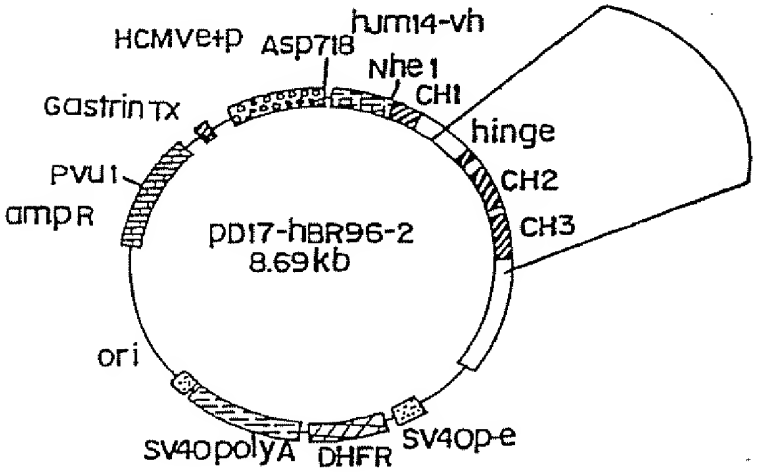


FIG. 13

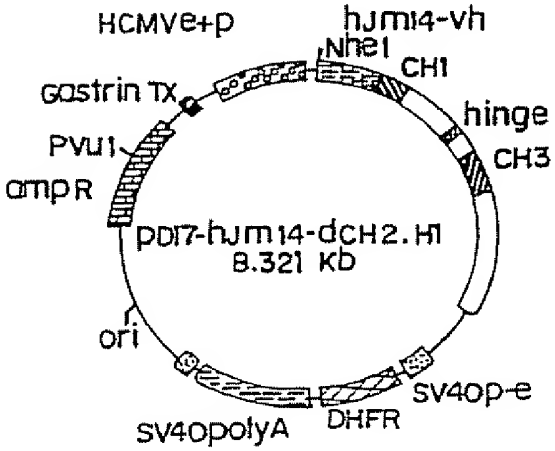


FIG. 14A
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

```
        10         20         30         40         50         60         70         80         90
GACGGATCGG GAGATCTGCT AGGTGACCTG AGGCGCGCCG GCTTCGAATA GCCAGAGTAA CCTTTTTTTT TAATTTTATT TTATTTTATT
CTGCCTAGCC CTCTAGACGA TCCACTGGAC TCCGCGCGGC CGAAGCTTAT CGGTCTCATT GGAAAAAAAA ATTAAAATAA AATAAAATAA

       100        110        120        130        140        150        160        170        180
TTTGAGATGG AGTTTGGCGC CGATCTCCCG ATCCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC
AAACTCTACC TCAAACCGCG GCTAGAGGGC TAGGGGATAC CAGCTGAGAG TCATGTTAGA CGAGACTACG GCGTATCAAT TCGGTCATAG

       190        200        210        220        230        240        250        260        270
TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGCGC GAGCAAAATT TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA
ACGAGGGACG AACACACAAC CTCCAGCGAC TCATCACGCG CTCGTTTTAA ATTCGATGTT GTTCCGTTCC GAACTGGCTG TTAACGTACT

       280        290        300        310        320        330        340        350        360
AGAATCTGCT TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC GTTGACATTG ATTATTGACT AGTTATTAAT
TCTTAGACGA ATCCCAATCC GCAAAACGCG ACGAAGCGCT ACATGCCCGG TCTATATGCG CAACTGTAAC TAATAACTGA TCAATAATTA

       370        380        390        400        410        420        430        440        450
AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC
TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGCG CAATGTATTG AATGCCATTT ACCGGGCGGA CCGACTGGCG

       460        470        480        490        500        510        520        530        540
CCAACGACCC CCGCCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA TGGGTGGACT
GGTTGCTGGG GGCGGGTAAC TGCAGTTATT ACTGCATACA AGGGTATCAT TGCGGTTATC CCTGAAAGGT AACTGCAGTT ACCCACCTGA

       550        560        570        580        590        600        610        620        630
ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG
TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA TTTACCGGGC

       640        650        660        670        680        690        700        710        720
CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
GGACCGTAAT ACGGGTCATG TACTGGAATA CCCTGAAAGG ATGAACCGTC ATGTAGATGC ATAATCAGTA GCGATAATGG TACCACTACG

       730        740        750        760        770        780        790        800        810
GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT
CCAAAACCGT CATGTAGTTA CCCGCACCTA TCGCCAAACT GAGTGCCCCT AAAGGTTCAG AGGTGGGGTA ACTGCAGTTA CCCTCAAACA

       820        830        840        850        860        870        880        890        900
TTTGGCACCA AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG
AAACCGTGGT TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG TTTACCCGCC ATCCGCACAT GCCACCCTCC
```

FIG. 14B

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

```
       910        920        930        940        950        960        970        980        990
TCTATATAAG CAGAGCTCTC TGGCTAACTA GAGAACCCAC TGCTTACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG
AGATATATTC GTCTCGAGAG ACCGATTGAT CTCTTGGGTG ACGAATGACC GAATAGCTTT AATTATGCTG AGTGATATCC CTCTGGGTTC

      1000       1010       1020       1030       1040       1050       1060       1070       1080
CTTGGTACCA ATTTAAATTG ATATCTCCTT AGGTCTCGAG TCTCTAGATA ACCGGTCAAT CGATTGGAAT TCTTGCGGCC GCTTGCTAGC
GAACCATGGT TAAATTTAAC TATAGAGGAA TCCAGAGCTC AGAGATCTAT TGGCCAGTTA GCTAACCTTA AGAACGCCGG CGAACGATCG

      1090       1100       1110       1120       1130       1140       1150       1160       1170
CACCATGGAG TTGTGGTTAA GCTTGGTCCT TCCTTGTCCT TGTTTTAAAA GGTGTCCAGT GTGAAGTGAA TCTGGTGGAG TCTGGGGGAG
GTGGTACCTC AACACCAATT CGAACCAGGA AGGAACAGGA ACAAAATTTT CCACAGGTCA CACTTCACTT AGACCACCTC AGACCCCCTC

      1180       1190       1200       1210       1220       1230       1240       1250       1260
GCTTAGTGCA GCCTGGAGGG TCCCTGAAAG TCTCCTGTGT AACCTCTGGA TTCACTTTCA GTGACTATTA CATGTATTGG GTTCGCCAGA
CGAATCACGT CGGACCTCCC AGGGACTTTC AGAGGACACA TTGGAGACCT AAGTGAAAGT CACTGATAAT GTACATAACC CAAGCGGTCT

      1270       1280       1290       1300       1310       1320       1330       1340       1350
CTCCAGAGAA GAGGCTGGAG TGGGTCGCAT ACATTAGTCA AGGTGGTGAT ATAACCGACT ATCCAGACAC TGTAAAGGGT CGATTCACCA
GAGGTCTCTT CTCCGACCTC ACCCAGCGTA TGTAATCAGT TCCACCACTA TATTGGCTGA TAGGTCTGTG ACATTTCCCA GCTAAGTGGT

      1360       1370       1380       1390       1400       1410       1420       1430       1440
TCTCCAGAGA CAATGCCAAG AACACCCTGT ACCTGCAAAT GAGCCGTCTG AAGTCTGAGG ACACAGCCAT GTATTACTGT GCAAGAGGCC
AGAGGTCTCT GTTACGGTTC TTGTGGGACA TGGACGTTTA CTCGGCAGAC TTCAGACTCC TGTGTCGGTA CATAATGACA CGTTCTCCGG

      1450       1460       1470       1480       1490       1500       1510       1520       1530
TGGACGACGG GGCCTGGTTT GCTTACTGGG GCCAAGGGAC TCTGGTCACG GTCTCTGTAG CTAGCACCAA GGGCCCATCG GTCTTCCCCC
ACCTGCTGCC CCGGACCAAA CGAATGACCC CGGTTCCCTG AGACCAGTGC CAGAGACATC GATCGTGGTT CCCGGGTAGC CAGAAGGGGG

      1540       1550       1560       1570       1580       1590       1600       1610       1620
TGGCACCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
ACCGTGGGAG GAGGTTCTCG TGGAGACCCC CGTGTCGCCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC TGCCACAGCA

      1630       1640       1650       1660       1670       1680       1690       1700       1710
GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTCACCG
CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCAGTGGC

      1720       1730       1740       1750       1760       1770       1780       1790       1800
TGCCCTCCAG CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA GTTGGTGAGA
ACGGGAGGTC GTCGAACCCG TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT CAACCACTCT
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FIG. 14C

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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1810  1820  1830  1840  1850  1860  1870  1880  1890
GGCCAGCACA GGGAGGGAGG GTGTCTGCTG GAAGCCAGGC TCAGCGCTCC TGCCTGGACG CATCCCGGCT ATGCAGCCCC AGTCCAGGGC
CCGGTCGTGT CCCTCCCTCC CACAGACGAC CTTCGGTCCG AGTCGCGAGG ACGGACCTGC GTAGGGCCGA TACGTCGGGG TCAGGTCCCG

1900  1910  1920  1930  1940  1950  1960  1970  1980
AGCAAGGCAG GCCCCGTCTG CCTCTTCACC CGGAGGCCTC TGCCCGCCCC ACTCATGCTC AGGGAGAGGG TCTTCTGGCT TTTTCCCCAG
TCGTTCCGTC CGGGGCAGAC GGAGAAGTGG GCCTCCGGAG ACGGGCGGGG TGAGTACGAG TCCCTCTCCC AGAAGACCGA AAAAGGGGTC

1990  2000  2010  2020  2030  2040  2050  2060  2070
GCTCTGGGCA GGCACAGGCT AGGTGCCCCT AACCCAGGCC CTGCACACAA AGGGGCAGGT GCTGGGCTCA GACCTGCCAA GAGCCATATC
CGAGACCCGT CCGTGTCCGA TCCACGGGGA TTGGGTCCGG GACGTGTGTT TCCCCGTCCA CGACCCGAGT CTGGACGGTT CTCGGTATAG

2080  2090  2100  2110  2120  2130  2140  2150  2160
CGGGAGGACC CTGCCCCTGA CCTAAGCCCA CCCCAAAGGC CAAACTCTCC ACTCCCTCAG CTCGGACACC TTCTCTCCTC CCAGATTCCA
GCCCTCCTGG GACGGGGACT GGATTCGGGT GGGGTTTCCG GTTTGAGAGG TGAGGGAGTC GAGCCTGTGG AAGAGAGGAG GGTCTAAGGT

2170  2180  2190  2200  2210  2220  2230  2240  2250
GTAACTCCCA ATCTTCTCTC TGCAGAGCCC AAATCTTGTG ACAAAACTCA CACATGCCCA CCGTGCCCAG GTAAGCCAGC CCAGGCCTCG
CATTGAGGGT TAGAAGAGAG ACGTCTCGGG TTTAGAACAC TGTTTTGAGT GTGTACGGGT GGCACGGGTC CATTCGGTCG GGTCCGGAGC

2260  2270  2280  2290  2300  2310  2320  2330  2340
CCCTCCAGCT CAAGGCGGGA CAGGTGCCCT AGAGTAGCCT GCATCCAGGG ACACACCACG TGGGTACCAA CATGTCCGGA GCCACATGGA
GGGAGGTCGA GTTCCGCCCT GTCCACGGGA TCTCATCGGA CGTAGGTCCC TGTGTGGTGC ACCCATGGTT GTACAGGCCT CGGTGTACCT

2350  2360  2370  2380  2390  2400  2410  2420  2430
CAGAGGCCGG CTCGGCCCAC CCTCTGCCCT GAGAGTGACC GCTGTACCAA CCTCTGTCCC TACAGGGCAG CCCCGAGAAC CACAGGTGTA
GTCTCCGGCC GAGCCGGGTG GGAGACGGGA CTCTCACTGG CGACATGGTT GGAGACAGGG ATGTCCCGTC GGGGCTCTTG GTGTCCACAT

2440  2450  2460  2470  2480  2490  2500  2510  2520
CACCCTGCCC CCATCCCGGG ATGAGCTGAC CAAGAACCAG GTCAGCCTGA CCTGCCTGGT CAAAGGCTTC TATCCCAGCG ACATCGCCGT
GTGGGACGGG GGTAGGGCCC TACTCGACTG GTTCTTGGTC CAGTCGGACT GGACGGACCA GTTTCCGAAG ATAGGGTCGC TGTAGCGGCA

2530  2540  2550  2560  2570  2580  2590  2600  2610
GGAGTGGGAG AGCAATGGGC AGCCGGAGAA CAACTACAAG ACCACGCCTC CCGTGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCAA
CCTCACCCTC TCGTTACCCG TCGGCCTCTT GTTGATGTTC TGGTGCGGAG GGCACGACCT GAGGCTGCCG AGGAAGAAGG AGATGTCGTT

2620  2630  2640  2650  2660  2670  2680  2690  2700
GCTCACCGTG GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG CACAACCACT ACACGCAGAA
CGAGTGGCAC CTGTTCTCGT CCACCGTCGT CCCCTTGCAG AAGAGTACGA GGCACTACGT ACTCCGAGAC GTGTTGGTGA TGTGCGTCTT
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FIG. 14D

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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2710        2720        2730        2740        2750        2760        2770        2780        2790
GAGCCTCTCC  CTGTCTCCGG  GTAAATGAGT  GCGACGGCCG  GCAAGCCCCC  GCTCCCCGGG  CTCTCGCGGT  CGCACGAGGA  TGCTTGGCAC
CTCGGAGAGG  GACAGAGGCC  CATTTACTCA  CGCTGCCGGC  CGTTCGGGGG  CGAGGGGCCC  GAGAGCGCCA  GCGTGCTCCT  ACGAACCGTG

2800        2810        2820        2830        2840        2850        2860        2870        880
GTACCCCCTG  TACATACTTC  CCGGGCGCCC  AGCATGGAAA  TAAAGCACCC  AGCGCTGCCC  TGGGCCCCTG  CGAGACTGTG  ATGGTTCTTT
CATGGGGGAC  ATGTATGAAG  GGCCCGCGGG  TCGTACCTTT  ATTTCGTGGG  TCGCGACGGG  ACCCGGGGAC  GCTCTGACAC  TACCAAGAAA

2890        2900        2910        2920        2930        2940        2950        2960        2970
CCACGGGTCA  GGCCGAGTCT  GAGGCCTGAG  TGGCATGAGG  GAGGCAGAGC  GGGTCCCACT  GTCCCCACAC  TGGCCCAGGC  TGTGCAGGTG
GGTGCCCAGT  CCGGCTCAGA  CTCCGGACTC  ACCGTACTCC  CTCCGTCTCG  CCCAGGGTGA  CAGGGGTGTG  ACCGGGTCCG  ACACGTCCAC

2980        2990        3000        3010        3020        3030        3040        3050        3060
TGCCTGGGCC  CCCTAGGGTG  GGGCTCAGCC  AGGGGCTGCC  CTCGGCAGGG  TGGGGGATTT  GCCAGCGTGG  CCCTCCCTCC  AGCAGCACCT
ACGGACCCGG  GGGATCCCAC  CCCGAGTCGG  TCCCCGACGG  GAGCCGTCCC  ACCCCCTAAA  CGGTCGCACC  GGGAGGGAGG  TCGTCGTGGA

3070        3080        3090        3100        3110        3120        3130        3140        3150
GCCCTGGGCT  GGGCCACGGG  AAGCCCTAGG  AGCCCCTGGG  GACAGACACA  CAGCCCCTGC  CTCTGTAGGA  GACTGTCCTG  TTCTGTGAGC
CGGGACCCGA  CCCGGTGCCC  TTCGGGGATCC  TCGGGGACCC  CTGTCTGTGT  GTCGGGGACG  GAGACATCCT  CTGACAGGAC  AAGACACTCG

3160        3170        3180        3190        3200        3210        3220        3230        3240
GCCCCTGTCC  TCCCGACCTC  CATGCCCACT  CGGGGGCATG  CCTAGTCCAT  GTGCGTAGGG  ACAGGCCCTC  CCTCACCCAT  CTACCCCCAC
CGGGGACAGG  AGGGCTGGAG  GTACGGGTGA  GCCCCCCGTAC  GGATCAGGTA  CACGCATCCC  TGTCCGGGAG  GGAGTGGGTA  GATGGGGGTG

3250        3260        3270        3280        3290        3300        3310        3320        3330
GGCACTAACC  CCTGGCTGCC  CTGCCCAGCC  TCGCACCCGC  ATGGGGACAC  AACCGACTCC  GGGGACATGC  ACTCTCGGGC  CCTGTGGAGG
CCGTGATTGG  GGACCGACGG  GACGGGTCGG  AGCGTGGGCG  TACCCCTGTG  TTGGCTGAGG  CCCCTGTACG  TGAGAGCCCG  GGACACCTCC

3340        3350        3360        3370        3380        3390        3400        3410        3420
GACTGGTGCA  GATGCCCACA  CACACACTCA  GCCCAGACCC  GTTCAACAAA  CCCCGCACTG  AGGTTGGCCG  GCCACACGGC  CACCACACAC
CTGACCACGT  CTACGGGTGT  GTGTGTGAGT  CGGGTCTGGG  CAAGTTGTTT  GGGGCGTGAC  TCCAACCGGC  CGGTGTGCCG  GTGGTGTGTG

3430        3440        3450        3460        3470        3480        3490        3500        3510
ACACGTGCAC  GCCTCACACA  CGGAGCCTCA  CCCGGGCGAA  CTGCACAGCA  CCCAGACCAG  AGCAAGGTCC  TCGCACACGT  GAACACTCCT
TGTGCACGTG  CGGAGTGTGT  GCCTCGGAGT  GGGCCCGCTT  GACGTGTCGT  GGGTCTGGTC  TCGTTCCAGG  AGCGTGTGCA  CTTGTGAGGA

3520        3530        3540        3550        3560        3570        3580        3590        3600
CGGACACAGG  CCCCCACGAG  CCCCACGCGG  CACCTCAAGG  CCCACGAGCC  TCTCGGCAGC  TTCTCCACAT  GCTGACCTGC  TCAGACAAAC
GCCTGTGTCC  GGGGGTGCTC  GGGGTGCGCC  GTGGAGTTCC  GGGTGCTCGG  AGAGCCGTCG  AAGAGGTGTA  CGACTGGACG  AGTCTGTTTG
```

FIG. 14E

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

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3610       3620       3630       3640       3650       3660       3670       3680       3690
CCAGCCCTCC TCTCACAAGG GTGCCCCTGC AGCCGCCACA CACACACAGG GGATCACACA CCACGTCACG TCCCTGGCCC TGGCCCACTT
GGTCGGGAGG AGAGTGTTCC CACGGGGACG TCGGCGGTGT GTGTGTGTCC CCTAGTGTGT GGTGCAGTGC AGGGACCGGG ACCGGGTGAA

3700       3710       3720       3730       3740       3750       3760       3770       3780
CCCAGTGCCG CCCTTCCCTG CAGGACGGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT
GGGTCACGGC GGGAAGGGAC GTCCTGCCTA GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA

3790       3800       3810       3820       3830       3840       3850       3860       3870
CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC
GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA GCGTAACAGA CTCATCCACA GTAAGATAAG

3880       3890       3900       3910       3920       3930       3940       3950       3960
TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG
ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCCTCCTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC

3970       3980       3990       4000       4010       4020       4030       4040       4050
AGGCGGAAAG AACCAGCTGG GGCTCTAGGG GGTATCCCCA CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA
TCCGCCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCGCGGGACA TCGCCGCCGTA ATTCGCGCCG CCCACACCAC CAATGCGCGT

4060       4070       4080       4090       4100       4110       4120       4130       4140
GCGTGACCGC TACACTTGCC AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGCCAC GTTCGCCGGG CCTCTCAAAA
CGCACTGGCG ATGTGAACGG TCGCGGGATC GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG CAAGCGGCCC GGAGAGTTTT

4150       4160       4170       4180       4190       4200       4210       4220       4230
AAGGGAAAAA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CTAACTCCGC CCATCCCGCC CCTAACTCCG CCCAGTTCCG
TTCCCTTTTT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GATTGAGGCG GGTAGGGCGG GGATTGAGGC GGGTCAAGGC

4240       4250       4260       4270       4280       4290       4300       4310       4320
CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTTATTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
GGGTAAGAGG CGGGGTACCG ACTGATTAAA AAAAATAAAT ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

4330       4340       4350       4360       4370       4380       4390       4400       4410
GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGG ACAGCTCAGG GCTGCGATTT CGCGCCAAAC TTGACGGCAA TCCTAGCGTG
CTCCGAAAAA ACCTCCGGAT CCGAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA GCGCGGTTTG AACTGCCGTT AGGATCGCAC

4420       4430       4440       4450       4460       4470       4480       4490       4500
AAGGCTGGTA GGATTTTATC CCCGCTGCCA TCATGGTTCG ACCATTGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
TTCCGACCAT CCTAAAATAG GGGCGACGGT AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT
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FIG. 14F

Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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      4510       4520       4530       4540       4550       4560       4570       4580       4590
ACGGAGACCT ACCCTGGCCT CCGCTCAGGA ACGAGTTCAA GTACTTCCAA AGAATGACCA CAACCTCTTC AGTGGAAGGT AAACAGAATC
TGCCTCTGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT GTTGGAGAAG TCACCTTCCA TTTGTCTTAG

      4600       4610       4620       4630       4640       4650       4660       4670       4680
TGGTGATTAT GGGTAGGAAA ACCTGGTTCT CCATTCCTGA GAAGAATCGA CCTTTAAAGG ACAGAATTAA TATAGTTCTC AGTAGAGAAC
ACCACTAATA CCCATCCTTT TGGACCAAGA GGTAAGGACT CTTCTTAGCT GGAAATTTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG

      4690       4700       4710       4720       4730       4740       4750       4760       4770
TCAAAGAACC ACCACGAGGA GCTCATTTTC TTGCCAAAAG TTTGGATGAT GCCTTAAGAC TTATTGAACA ACCGGAATTG GCAAGTAAAG
AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG AATAACTTGT TGGCCTTAAC CGTTCATTTC

      4780       4790       4800       4810       4820       4830       4840       4850       4860
TAGACATGGT TTGGATAGTC GGAGGCAGTT CTGTTTACCA GGAAGCCATG AATCAACCAG GCCACCTTAG ACTCTTTGTG ACAAGGATCA
ATCTGTACCA AACCTATCAG CCTCCGTCAA GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT

      4870       4880       4890       4900       4910       4920       4930       4940       4950
TGCAGGAATT TGAAAGTGAC ACGTTTTTCC CAGAAATTGA TTTGGGGAAA TATAAACTTC TCCCAGAATA CCCAGGCGTC CTCTCTGAGG
ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG AGGGTCTTAT GGGTCCGCAG GAGAGACTCC

      4960       4970       4980       4990       5000       5010       5020       5030       5040
TCCAGGAGGA AAAAGGCATC AAGTATAAGT TTGAAGTCTA CGAGAAGAAA GACTAACAGG AAGATGCTTT CAAGTTCTCT GCTCCCCTCC
AGGTCCTCCT TTTTCCGTAG TTCATATTCA AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG

      5050       5060       5070       5080       5090       5100       5110       5120       5130
TAAAGCTATG CATTTTTATA AGACCATGGG ACTTTTGCTG GCTTTAGATC TCTTTGTGAA GGAACCTTAC TTCTGTGGTG TGACATAATT
ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT CCTTGGAATG AAGACACCAC ACTGTATTAA

      5140       5150       5160       5170       5180       5190       5200       5210       5220
GGACAAACTA CCTACAGAGA TTTAAAGCTC TAAGGTAAAT ATAAAATTTT TAAGTGTATA ATGTGTTAAA CTACTGATTC TAATTGTTTG
CCTGTTTGAT GGATGTCTCT AAATTTCGAG ATTCCATTTA TATTTTAAAA ATTCACATAT TACACAATTT GATGACTAAG ATTAACAAAC

      5230       5240       5250       5260       5270       5280       5290       5300       5310
TGTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT
ACATAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT ACTCCTTTTG GACAAAACGA GTCTTCTTTA

      5320       5330       5340       5350       5360       5370       5380       5390       5400
GCCATCTAGT GATGATGAGG CTACTGCTGA CTCTCAACAT TCTACTCCTC CAAAAAAGAA GAGAAAGGTA GAAGACCCCA AGGACTTTCC
CGGTAGATCA CTACTACTCC GATGACGACT GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTCCAT CTTCTGGGGT TCCTGAAAGG
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FIG. 14G
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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      5410       5420       5430       5440       5450       5460       5470       5480       5490
TTCAGAATTG CTAAGTTTTT TGAGTCATGC TGTGTTTAGT AATAGAACTC TTGCTTGCTT TGCTATTTAC ACCACAAAGG AAAAAGCTGC
AAGTCTTAAC GATTCAAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGAACGAA ACGATAAATG TGGTGTTTCC TTTTTCGACG

      5500       5510       5520       5530       5540       5550       5560       5570       5580
ACTGCTATAC AAGAAAATTA TGGAAAAATA TTCTGTAACC TTTATAAGTA GGCATAACAG TTATAATCAT AACATACTGT TTTTTCTTAC
TGACGATATG TTCTTTTAAT ACCTTTTTAT AAGACATTGG AAATATTCAT CCGTATTGTC AATATTAGTA TTGTATGACA AAAAAGAATG

      5590       5600       5610       5620       5630       5640       5650       5660       5670
TCCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAATTGT GTACCTTTAG CTTTTTAATT TGTAAAGGGG TTAATAAGGA
AGGTGTGTCC GTATCTCACA GACGATAATT ATTGATACGA GTTTTTAACA CATGGAAATC GAAAAATTAA ACATTTCCCC AATTATTCCT

      5680       5690       5700       5710       5720       5730       5740       5750       5760
ATATTTGATG TATAGTGCCT TGACTAGAGA TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC
TATAAACTAC ATATCACGGA ACTGATCTCT AGTATTAGTC GGTATGGTGT AAACATCTCC AAAATGAACG AAATTTTTTG GAGGGTGTGG

      5770       5780       5790       5800       5810       5820       5830       5840       5850
TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACTTG TTTATTGCAG CTTATAATGG TTACAAATAA AGCAATAGCA
AGGGGGACTT GGACTTTGTA TTTTACTTAC GTTAACAACA ACAATTGAAC AAATAACGTC GAATATTACC AATGTTTATT TCGTTATCGT

      5860       5870       5880       5890       5900       5910       5920       5930       5940
TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTGGATCG
AGTGTTTAAA GTGTTTATTT CGTAAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

      5950       5960       5970       5980       5990       6000       6010       6020       6030
GCTGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT TTATTGCAGC TTATAATGGT TACAAATAAA
CGACCTACTA GGAGGTCGCG CCCCTAGAGT ACGACCTCAA GAAGCGGGTG GGGTTGAACA AATAACGTCG AATATTACCA ATGTTTATTT

      6040       6050       6060       6070       6080       6090       6100       6110       6120
GCAATAGCAT CACAAATTTC ACAAATAAAG CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG
CGTTATCGTA GTGTTTAAAG TGTTTATTTC GTAAAAAAAG TGACGTAAGA TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC

      6130       6140       6150       6160       6170       6180       6190       6200       6210
TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC
AGACATATGG CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAGTATC GACAAAGGAC ACACTTTAAC AATAGGCGAG TGTTAAGGTG

      6220       6230       6240       6250       6260       6270       6280       6290       6300
ACAACATACG AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
TGTTGTATGC TCGGCCTTCG TATTTCACAT TTCGGACCCC ACGGATTACT CACTCGATTG AGTGTAATTA ACGCAACGCG AGTGACGGGC
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FIG. 14H

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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      6310       6320       6330       6340       6350       6360       6370       6380       6390
CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA GAGGCGGTTT GCGTATTGGG CGCTCTTCCG
GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCGCGCCCCT CTCCGCCAAA CGCATAACCC GCGAGAAGGC

      6400       6410       6420       6430       6440       6450       6460       6470       6480
CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

      6490       6500       6510       6520       6530       6540       6550       6560       6570
AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC
TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG

      6580       6590       6600       6610       6620       6630       6640       6650       6660
ATAGGCTCCG CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
TATCCGAGGC GGGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCAGTC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

      6670       6680       6690       6700       6710       6720       6730       6740       6750
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG
AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ACAGGCGGAA AGAGGGAAGC CCTTCGCACC

      6760       6770       6780       6790       6800       6810       6820       6830       6840
CGCTTTCTCA ATGCTCACGC TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
GCGAAAGAGT TACGAGTGCG ACATCCATAG AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG

      6850       6860       6870       6880       6890       6900       6910       6920       6930
CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT

      6940       6950       6960       6970       6980       6990       7000       7010       7020
GGATTAGCAG AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC ACCGGATTGA TGCCGATGTG ATCTTCCTGT CATAAACCAT

      7030       7040       7050       7060       7070       7080       7090       7100       7110
TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT
AGACGCGAGA CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT TTGTTTGGTG GCGACCATCG CCACCAAAAA

      7120       7130       7140       7150       7160       7170       7180       7190       7200
TTGTTTGCAA GCAGCAGATT ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
AACAAACGTT CGTCGTCTAA TGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC CAGACTGCGA GTCACCTTGC
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FIG. 14I

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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      7210       7220       7230       7240       7250       7260       7270       7280       7290
AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT TTTAAATCAA
TTTTGAGTGC AATTCCCTAA AACCAGTACT CTAATAGTTT TTCCTAGAAG TGGATCTAGG AAAATTTAAT TTTTACTTCA AAATTTAGTT

      7300       7310       7320       7330       7340       7350       7360       7370       7380
TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT
AGATTTCATA TATACTCATT TGAACCAGAC TGTCAATGGT TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT AAAGCAAGTA

      7390       7400       7410       7420       7430       7440       7450       7460       7470
CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC
GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG AATGGTAGAC CGGGGTCACG ACGTTACTAT GGCGCTCTGG

      7480       7490       7500       7510       7520       7530       7540       7550       7560
CACGCTCACC GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA
GTGCGAGTGG CCGAGGTCTA AATAGTCGTT ATTTGGTCGG TCGGCCTTCC CGGCTCGCGT CTTCACCAGG ACGTTGAAAT AGGCGGAGGT

      7570       7580       7590       7600       7610       7620       7630       7640       7650
TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT ACAGGCATCG
AGGTCAGATA ATTAACAACG GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG CGTTGCAACA ACGGTAACGA TGTCCGTAGC

      7660       7670       7680       7690       7700       7710       7720       7730       7740
TGGTGTCACG CTCGTCGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA
ACCACAGTGC GAGCAGCAAA CCATACCGAA GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC AACACGTTTT

      7750       7760       7770       7780       7790       7800       7810       7820       7830
AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT GACGTATTAA

      7840       7850       7860       7870       7880       7890       7900       7910       7920
CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA
GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG ACCACTCATG AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT

      7930       7940       7950       7960       7970       7980       7990       8000       8010
GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGGC
CAACGAGAAC GGGCCGCAGT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAAATTTTC ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG

      8020       8030       8040       8050       8060       8070       8080       8090       8100
GAAAACTCTC AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
CTTTTGAGAG TTCCTAGAAT GGCGACAACT CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGTAGA AAATGAAAGT
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FIG. 14J
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

pD17-cJ-dCH2.H1

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      8110       8120       8130       8140       8150       8160       8170       8180       8190
CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT
GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT GAGTATGAGA

      8200       8210       8220       8230       8240       8250       8260       8270       8280
TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

      8290       8300       8310       8320       8330
GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT C
CCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA G
```

FIG. 15

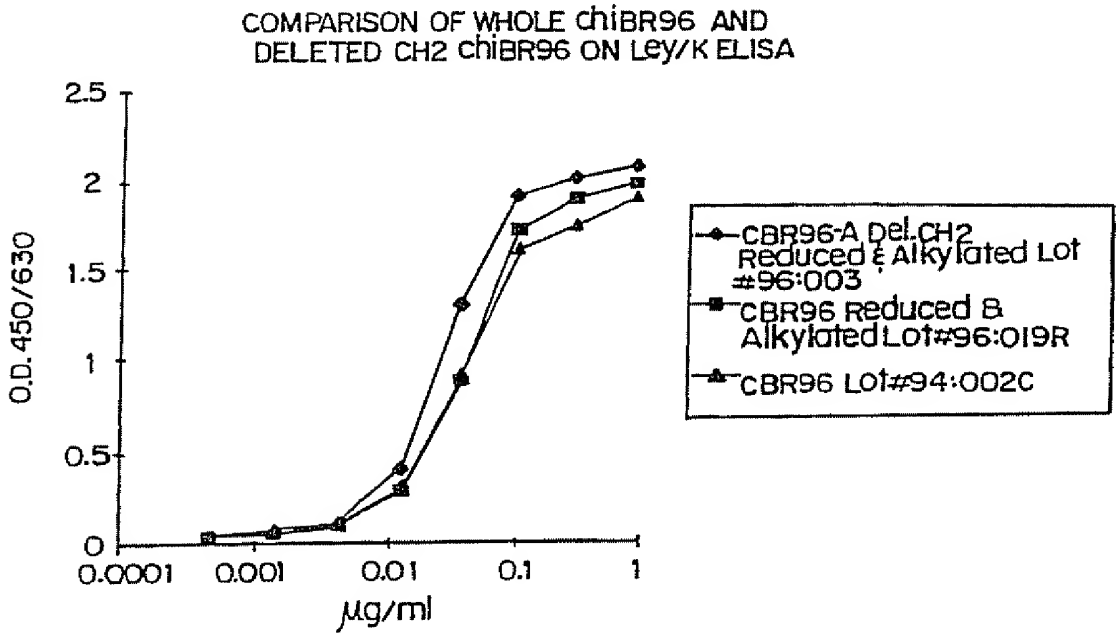
COMPARISON OF WHOLE chiBR96 AND
DELETED CH2 chiBR96 ON Ley/K ELISA
O.D. 450/630
2.5
2
1.5
1
0.5
0
0.0001
0.001
0.01
0.1
1
µg/ml
CBR96-A Del.CH2 Reduced & Alkylated Lot #96:003
CBR96 Reduced & Alkylated Lot#96:019R
CBR96 Lot#94:002C

FIG. 16

hBR96-2B:L235 to A235 and G237 to A237

hBR96-2C:E318 to S318, K320 to S320, and K322 to S322

hBR96-2D:P331 to A331

hBR96-2E:L235 to A235, G237 to A237, E318 to S318, K320 to S320, and K322 to S322

hBR96-2F:L235 to A235, G237 to A237, and P331 to A331

hBR96-2G:E318 to S318, K320 to S320, K322 to S322, and P331 to A331

hBR96-2H: L235 to A235, G237 to A237, E318 to S318, K320 to S320, K322 to S322, and P331 to A331

FIG. 17

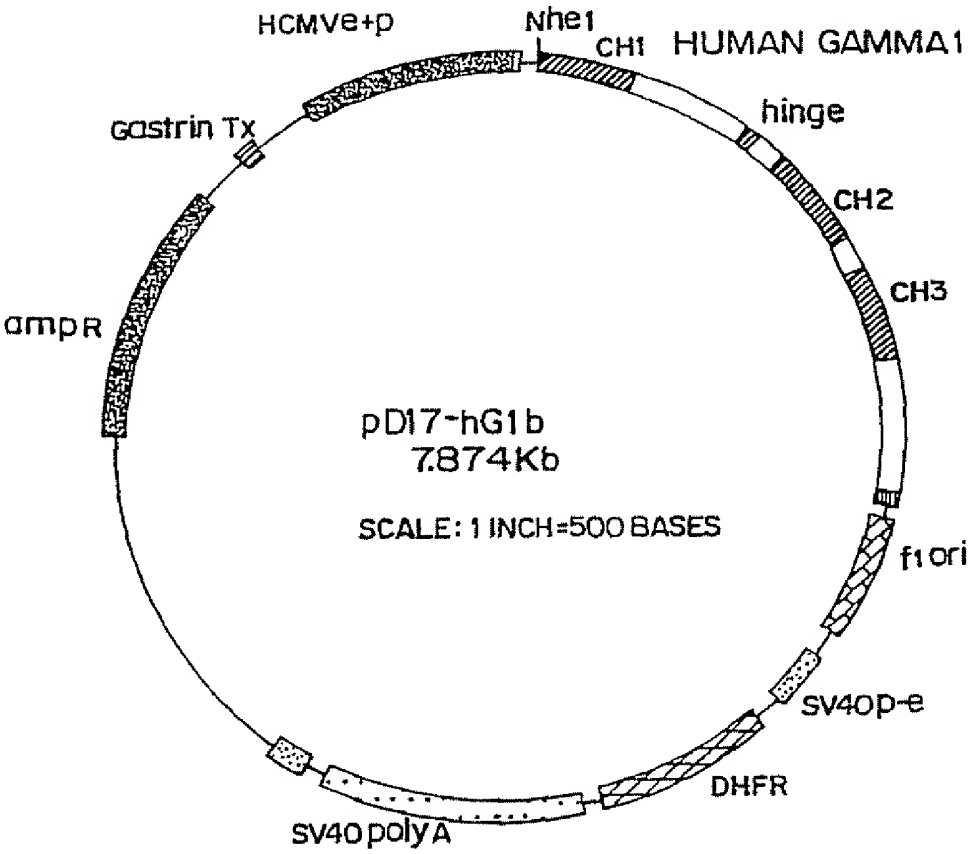
HCMVe+p
Nhe1
CH1
HUMAN GAMMA1
hinge
CH2
CH3
f1 ori
SV40p-e
DHFR
SV40 polyA
ampR
Gastrin Tx
pD17-hG1b
7.874Kb
SCALE: 1 INCH=500 BASES

FIG. 18A

(SEQ ID NO:22)

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   1 GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC
  51 GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG
 101 TGGTTAAGCT TGGTCTTCCT TGTCCTTGTT TTAAAAGGTG TCCAGTGTGA
 151 AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC
 201 TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG
 251 TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT
 301 TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT
 351 TCACCATCTC CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC
 401 AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC
 451 GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT
 501 CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
 551 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA
 601 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG
 651 GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
 701 AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT
 751 CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG
 801 GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG
 851 CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA
 901 AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC
 951 ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA
1001 CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG
1051 GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA
1101 AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT
1151 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT
1201 CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG
1251 GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT
1301 CCAGGGACAG GCCCCAGCCG GGTGCTGACA CGTCCACCTC CATCTCTTCC
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FIG. 18B

(SEQ ID NO:22)

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                                235       237
1351 TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA
1401 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG
1451 TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
1501 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA
1551 CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
                          318       320   322
1601 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA
                331
1651 GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGGT
1701 GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA
1751 GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC GAGAACCACA
1801 GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA
1851 GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1901 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT
1951 GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA
2001 AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG
2051 GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA
2101 ATGAGTGCGA CGGCCGGCAA GCCCCCGCTC CCCGGGCTCT CGCGGTCGCA
2151 CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA
2201 TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG
2251 TTCTTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG
2301 CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC
2351 TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG GCTGCCCTCG GCAGGGTGGG
2401 GGATTTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCCC TGGGCTGGGC
2451 CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT
2501 GTAGGAGACT GTCCTGTTCT GTGAGCGCCC CTGTCCTCCC GACCTCCATG
2551 CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC
2601 ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC
2651 ACCCGCATGG GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG
2701 TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTTC
2751 AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC
2801 GTGCACGCCT CACACACGGA GCCTCACCCG GGCGAACTGC ACAGCACCCA
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FIG. 18C

(SEQ ID NO:22)

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2851 GACCAGAGCA  AGGTCCTCGC  ACACGTGAAC  ACTCCTCGGA  CACAGGCCCC
2901 CACGAGCCCC  ACGCGGCACC  TCAAGGCCCA  CGAGCCTCTC  GGCAGCTTCT
2951 CCACATGCTG  ACCTGCTCAG  ACAAACCCAG  CCCTCCTCTC  ACAAGGGTGC
3001 CCCTGCAGCC  GCCACACACA  CACAGGGGAT  CACACACCAC  GTCACGTCCC
3051 TGGCCCTGGC  CCACTTCCCA  GTGCCGCCCT  TCCCTGCAGG  ACGGATCAGC
3101 CTCGACTGTG  CCTTCTAGTT  GCCAGCCATC  TGTTGTTTGC  CCCTCCCCCG
3151 TGCCTTCCTT  GACCCTGGAA  GGTGCCACTC  CCACTGTCCT  TTCCTAATAA
3201 AATGAGGAAA  TTGCATCGCA  TTGTCTGAGT  AGGTGTCATT  CTATTCTGGG
3251 GGGTGGGGTG  GGGCAGGACA  GCAAGGGGGA  GGATTGGGAA  GACAATAGCA
3301 GGCATGCTGG  GGATGCGGTG  GGCTCTATGG  CTTCTGAGGC  GGAAAGAACC
3351 AGCTGGGGCT  CTAGGGGGTA  TCCCCACGCG  CCCTGTAGCG  GCGCATTAAG
3401 CGCGGCGGGT  GTGGTGGTTA  CGCGCAGCGT  GACCGCTACA  CTTGCCAGCG
3451 CCCTAGCGCC  CGCTCCTTTC  GCTTTCTTCC  CTTCCTTTCT  CGCCACGTTC
3501 GCCGGGCCTC  TCAAAAAAGG  GAAAAAAAGC  ATGCATCTCA  ATTAGTCAGC
3551 AACCATAGTC  CCGCCCCTAA  CTCCGCCCAT  CCCGCCCCTA  ACTCCGCCCA
3601 GTTCCGCCCA  TTCTCCGCCC  CATGGCTGAC  TAATTTTTTT  TATTTATGCA
3651 GAGGCCGAGG  CCGCCTCGGC  CTCTGAGCTA  TTCCAGAAGT  AGTGAGGAGG
3701 CTTTTTTGGA  GGCCTAGGCT  TTTGCAAAAA  GCTTGGACAG  CTCAGGGCTG
3751 CGATTTCGCG  CCAAACTTGA  CGGCAATCCT  AGCGTGAAGG  CTGGTAGGAT
3801 TTTATCCCCG  CTGCCATCAT  GGTTCGACCA  TTGAACTGCA  TCGTCGCCGT
3851 GTCCCAAAAT  ATGGGGATTG  GCAAGAACGG  AGACCTACCC  TGGCCTCCGC
3901 TCAGGAACGA  GTTCAAGTAC  TTCCAAAGAA  TGACCACAAC  CTCTTCAGTG
3951 GAAGGTAAAC  AGAATCTGGT  GATTATGGGT  AGGAAAACCT  GGTTCTCCAT
4001 TCCTGAGAAG  AATCGACCTT  TAAAGGACAG  AATTAATATA  GTTCTCAGTA
4051 GAGAACTCAA  AGAACCACCA  CGAGGAGCTC  ATTTTCTTGC  CAAAAGTTTG
4101 GATGATGCCT  TAAGACTTAT  TGAACAACCG  GAATTGGCAA  GTAAAGTAGA
4151 CATGGTTTGG  ATAGTCGGAG  GCAGTTCTGT  TTACCAGGAA  GCCATGAATC
4201 AACCAGGCCA  CCTTAGACTC  TTTGTGACAA  GGATCATGCA  GGAATTTGAA
4251 AGTGACACGT  TTTTCCCAGA  AATTGATTTG  GGGAAATATA  AACTTCTCCC
4301 AGAATACCCA  GGCGTCCTCT  CTGAGGTCCA  GGAGGAAAAA  GGCATCAAGT
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FIG. 18D

(SEQ ID NO:22)

4351	ATAAGTTTGA	AGTCTACGAG	AAGAAAGACT	AACAGGAAGA	TGCTTTCAAG
4401	TTCTCTGCTC	CCCTCCTAAA	GCTATGCATT	TTTATAAGAC	CATGGGACTT
4451	TTGCTGGCTT	TAGATCTCTT	TGTGAAGGAA	CCTTACTTCT	GTGGTGTGAC
4501	ATAATTGGAC	AAACTACCTA	CAGAGATTTA	AAGCTCTAAG	GTAAATATAA
4551	AATTTTTAAG	TGTATAATGT	GTTAAACTAC	TGATTCTAAT	TGTTTGTGTA
4601	TTTTAGATTC	CAACCTATGG	AACTGATGAA	TGGGAGCAGT	GGTGGAATGC
4651	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	AGAAATGCCA	TCTAGTGATG
4701	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	AAAGAAGAGA
4751	AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTTGAG
4801	TCATGCTGTG	TTTAGTAATA	GAACTCTTGC	TTGCTTTGCT	ATTTACACCA
4851	CAAAGGAAAA	AGCTGCACTG	CTATACAAGA	AAATTATGGA	AAAATATTCT
4901	GTAACCTTTA	TAAGTAGGCA	TAACAGTTAT	AATCATAACA	TACTGTTTTT
4951	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	TATTAATAAC	TATGCTCAAA
5001	AATTGTGTAC	CTTTAGCTTT	TTAATTTGTA	AAGGGGTTAA	TAAGGAATAT
5051	TTGATGTATA	GTGCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTTG
5101	TAGAGGTTTT	ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG
5151	AAACATAAAA	TGAATGCAAT	TGTTGTTGTT	AACTTGTTTA	TTGCAGCTTA
5201	TAATGGTTAC	AAATAAAGCA	ATAGCATCAC	AAATTTCACA	AATAAAGCAT
5251	TTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	CAATGTATCT
5301	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGGG	ATCTCATGCT
5351	GGAGTTCTTC	GCCCACCCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA
5401	AATAAAGCAA	TAGCATCACA	AATTTCACAA	ATAAAGCATT	TTTTTCACTG
5451	CATTCTAGTT	GTGGTTTGTC	CAAACTCATC	AATGTATCTT	ATCATGTCTG
5501	TATACCGTCG	ACCTCTAGCT	AGAGCTTGGC	GTAATCATGG	TCATAGCTGT
5551	TTCCTGTGTG	AAATTGTTAT	CCGCTCACAA	TTCCACACAA	CATACGAGCC
5601	GGAAGCATAA	AGTGTAAAGC	CTGGGGTGCC	TAATGAGTGA	GCTAACTCAC
5651	ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT
5701	GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT
5751	ATTGGGCGCT	CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT
5801	TCGGCTGCGG	CGAGCGGTAT	CAGCTCACTC	AAAGGCGGTA	ATACGGTTAT

FIG. 18E

(SEQ ID NO:22)

5851	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	ACATGTGAGC	AAAAGGCCAG
5901	CAAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTTCCATAG
5951	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT
6001	GGCGAAACCC	GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC
6051	TCCCTCGTGC	GCTCTCCTGT	TCCGACCCTG	CCGCTTACCG	GATACCTGTC
6101	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT	TTCTCAATGC	TCACGCTGTA
6151	GGTATCTCAG	TTCGGTGTAG	GTCGTTCGCT	CCAAGCTGGG	CTGTGTGCAC
6201	GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	TTATCCGGTA	ACTATCGTCT
6251	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG
6301	GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG
6351	AAGTGGTGGC	CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG
6401	CGCTCTGCTG	AAGCCAGTTA	CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT
6451	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	GTTTTTTTGT	TTGCAAGCAG
6501	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	TGATCTTTTC
6551	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	GGGATTTTGG
6601	TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAA
6651	TGAAGTTTTA	AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG
6701	TTACCAATGC	TTAATCAGTG	AGGCACCTAT	CTCAGCGATC	TGTCTATTTC
6751	GTTCATCCAT	AGTTGCCTGA	CTCCCCGTCG	TGTAGATAAC	TACGATACGG
6801	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	GAGACCCACG
6851	CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG
6901	AGCGCAGAAG	TGGTCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAT
6951	TGTTGCCGGG	AAGCTAGAGT	AAGTAGTTCG	CCAGTTAATA	GTTTGCGCAA
7001	CGTTGTTGCC	ATTGCTACAG	GCATCGTGGT	GTCACGCTCG	TCGTTTGGTA
7051	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	CAAGGCGAGT	TACATGATCC
7101	CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTCGGTCCTC	CGATCGTTGT
7151	CAGAAGTAAG	TTGGCCGCAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC
7201	ATAATTCTCT	TACTGTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT
7251	GAGTACTCAA	CCAAGTCATT	CTGAGAATAG	TGTATGCGGC	GACCGAGTTG
7301	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC	CGCGCCACAT	AGCAGAACTT

FIG. 18F

(SEQ ID NO:22)

7351	TAAAAGTGCT	CATCATTGGA	AAACGTTCTT	CGGGGCGAAA	ACTCTCAAGG
7401	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	GTGCACCCAA
7451	CTGATCTTCA	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA
7501	CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT
7551	TGAATACTCA	TACTCTTCCT	TTTTCAATAT	TATTGAAGCA	TTTATCAGGG
7601	TTATTGTCTC	ATGAGCGGAT	ACATATTTGA	ATGTATTTAG	AAAAATAAAC
7651	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	AAGTGCCACC	TGACGTCGAC
7701	GGATCGGGAG	ATCTGCTAGG	TGACCTGAGG	CGCGCCGGCT	TCGAATAGCC
7751	AGAGTAACCT	TTTTTTTTAA	TTTTATTTTA	TTTTATTTTT	GAGATGGAGT
7801	TTGGCGCCGA	TCTCCCGATC	CCCTATGGTC	GACTCTCAGT	ACAATCTGCT
7851	CTGATGCCGC	ATAGTTAAGC	CAGTATCTGC	TCCCTGCTTG	TGTGTTGGAG
7901	GTCGCTGAGT	AGTGCGCGAG	CAAAATTTAA	GCTACAACAA	GGCAAGGCTT
7951	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	GGTTAGGCGT	TTTGCGCTGC
8001	TTCGCGATGT	ACGGGCCAGA	TATACGCGTT	GACATTGATT	ATTGACTAGT
8051	TATTAATAGT	AATCAATTAC	GGGGTCATTA	GTTCATAGCC	CATATATGGA
8101	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	CCCGCCTGGC	TGACCGCCCA
8151	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	CATAGTAACG
8201	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGACTATT	TACGGTAAAC
8251	TGCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA
8301	TTGACGTCAA	TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG
8351	ACCTTATGGG	ACTTTCCTAC	TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC
8401	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	CATCAATGGG	CGTGGATAGC
8451	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTGA	CGTCAATGGG
8501	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA
8551	CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT
8601	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	TTACTGGCTT
8651	ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT	

FIG. 19A
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

10	20	30	40	50	60
GGTACCAATT	TAAATTGATA	TCTCCTTAGG	TCTCGAGTCT	CTAGATAACC	GGTCAATCGA
CCATGGTTAA	ATTTAACTAT	AGAGGAATCC	AGAGCTCAGA	GATCTATTGG	CCAGTTAGCT
70	80	90	100	110	120
TTGGAATTCT	TGCGGCCGCT	TGCTAGCACC	AAGGGCCCAT	CGGTCTTCCC	CCTGGCACCC
AACCTTAAGA	ACGCCGGCGA	ACGATCGTGG	TTCCCGGGTA	GCCAGAAGGG	GGACCGTGGG
130	140	150	160	170	180
TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG	GCCCTGGGCT	GCCTGGTCAA	GGACTACTTC
AGGAGGTTCT	CGTGGAGACC	CCCGTGTCGC	CGGGACCCGA	CGGACCAGTT	CCTGATGAAG
190	200	210	220	230	240
CCCGAACCGG	TGACGGTGTC	GTGGAACTCA	GGCGCCCTGA	CCAGCGGCGT	GCACACCTTC
GGGCTTGGCC	ACTGCCACAG	CACCTTGAGT	CCGCGGGACT	GGTCGCCGCA	CGTGTGGAAG
250	260	270	280	290	300
CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC	TCCCTCAGCA	GCGTGGTCAC	CGTGCCCTCC
GGCCGACAGG	ATGTCAGGAG	TCCTGAGATG	AGGGAGTCGT	CGCACCAGTG	GCACGGGAGG
310	320	330	340	350	360
AGCAGCTTGG	GCACCCAGAC	CTACATCTGC	AACGTGAATC	ACAAGCCCAG	CAACACCAAG
TCGTCGAACC	CGTGGGTCTG	GATGTAGACG	TTGCACTTAG	TGTTCGGGTC	GTTGTGGTTC
370	380	390	400	410	420
GTGGACAAGA	AAGTTGGTGA	GAGGCCAGCA	CAGGGAGGGA	GGGTGTCTGC	TGGAAGCCAG
CACCTGTTCT	TTCAACCACT	CTCCGGTCGT	GTCCCTCCCT	CCCACAGACG	ACCTTCGGTC
430	440	450	460	470	480
GCTCAGCGCT	CCTGCCTGGA	CGCATCCCGG	CTATGCAGCC	CCAGTCCAGG	GCAGCAAGGC
CGAGTCGCGA	GGACGGACCT	GCGTAGGGCC	GATACGTCGG	GGTCAGGTCC	CGTCGTTCCG
490	500	510	520	530	540
AGGCCCCGTC	TGCCTCTTCA	CCCGGAGGCC	TCTGCCCGCC	CCACTCATGC	TCAGGGAGAG
TCCGGGGCAG	ACGGAGAAGT	GGGCCTCCGG	AGACGGGCGG	GGTGAGTACG	AGTCCCTCTC
550	560	570	580	590	600
GGTCTTCTGG	CTTTTTCCCC	AGGCTCTGGG	CAGGCACAGG	CTAGGTGCCC	CTAACCCAGG
CCAGAAGACC	GAAAAAGGGG	TCCGAGACCC	GTCCGTGTCC	GATCCACGGG	GATTGGGTCC

FIG. 19B

Primary Sequence = SEQ ID NO:23

Complementary Sequence = SEQ ID NO:29

pD17-hG1b

610	620	630	640	650	660
CCCTGCACAC	AAAGGGGCAG	GTGCTGGGCT	CAGACCTGCC	AAGAGCCATA	TCCGGGAGGA
GGGACGTGTG	TTTCCCCGTC	CACGACCCGA	GTCTGGACGG	TTCTCGGTAT	AGGCCCTCCT
670	680	690	700	710	720
CCCTGCCCCT	GACCTAAGCC	CACCCCAAAG	GCCAAACTCT	CCACTCCCTC	AGCTCGGACA
GGGACGGGGA	CTGGATTCGG	GTGGGGTTTC	CGGTTTGAGA	GGTGAGGGAG	TCGAGCCTGT
730	740	750	760	770	780
CCTTCTCTCC	TCCCAGATTC	CAGTAACTCC	CAATCTTCTC	TCTGCAGAGC	CCAAATCTTG
GGAAGAGAGG	AGGGTCTAAG	GTCATTGAGG	GTTAGAAGAG	AGACGTCTCG	GGTTTAGAAC
790	800	810	820	830	840
TGACAAAACT	CACACATGCC	CACCGTGCCC	AGGTAAGCCA	GCCCAGGCCT	CGCCCTCCAG
ACTGTTTTGA	GTGTGTACGG	GTGGCACGGG	TCCATTCGGT	CGGGTCCGGA	GCGGGAGGTC
850	860	870	880	890	900
CTCAAGGCGG	GACAGGTGCC	CTAGAGTAGC	CTGCATCCAG	GGACAGGCCC	CAGCCGGGTG
GAGTTCCGCC	CTGTCCACGG	GATCTCATCG	GACGTAGGTC	CCTGTCCGGG	GTCGGCCCAC
910	920	930	940	235 237 950	960
CTGACACGTC	CACCTCCATC	TCTTCCTCAG	CACCTGAACT	CCTGGGGGGA	CCGTCAGTCT
GACTGTGCAG	GTGGAGGTAG	AGAAGGAGTC	GTGGACTTGA	GGACCCCCCT	GGCAGTCAGA
970	980	990	1000	1010	1020
TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	GAGGTCACAT
AGGAGAAGGG	GGGTTTTGGG	TTCCTGTGGG	AGTACTAGAG	GGCCTGGGGA	CTCCAGTGTA
1030	1040	1050	1060	1070	1080
GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	TACGTGGACG
CGCACCACCA	CCTGCACTCG	GTGCTTCTGG	GACTCCAGTT	CAAGTTGACC	ATGCACCTGC
1090	1100	1110	1120	1130	1140
GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	AGCACGTACC
CGCACCTCCA	CGTATTACGG	TTCTGTTTCG	GCGCCCTCCT	CGTCATGTTG	TCGTGCATGG
1150	1160	1170	1180	1190	318 320 1200
GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	GAGTACAAGT
CACACCAGTC	GCAGGAGTGG	CAGGACGTGG	TCCTGACCGA	CTTACCGTTC	CTCATGTTCA

FIG. 19C
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

FIG. 19D
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

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1810                1820                1830                1840                1850                1860
CCTGGGCCCC          TGCGAGACTG          TGATGGTTCT          TTCCACGGGT          CAGGCCGAGT          CTGAGGCCTG
GGACCCGGGG          ACGCTCTGAC          ACTACCAAGA          AAGGTGCCCA          GTCCGGCTCA          GACTCCGGAC

1870                1880                1890                1900                1910                1920
AGTGGCATGA          GGGAGGCAGA          GCGGGTCCCA          CTGTCCCCAC          ACTGGCCCAG          GCTGTGCAGG
TCACCGTACT          CCCTCCGTCT          CGCCCAGGGT          GACAGGGGTG          TGACCGGGTC          CGACACGTCC

1930                1940                1950                1960                1970                1980
TGTGCCTGGG          CCCCCTAGGG          TGGGGCTCAG          CCAGGGGCTG          CCCTCGGCAG          GGTGGGGGAT
ACACGGACCC          GGGGGATCCC          ACCCCGAGTC          GGTCCCCGAC          GGGAGCCGTC          CCACCCCCTA

1990                2000                2010                2020                2030                2040
TTGCCAGCGT          GGCCCTCCCT          CCAGCAGCAC          CTGCCCTGGG          CTGGGCCACG          GGAAGCCCTA
AACGGTCGCA          CCGGGAGGGA          GGTCGTCGTG          GACGGGACCC          GACCCGGTGC          CCTTCGGGAT

2050                2060                2070                2080                2090                2100
GGAGCCCCTG          GGGACAGACA          CACAGCCCCT          GCCTCTGTAG          GAGACTGTCC          TGTTCTGTGA
CCTCGGGGAC          CCCTGTCTGT          GTGTCGGGGA          CGGAGACATC          CTCTGACAGG          ACAAGACACT

2110                2120                2130                2140                2150                2160
GCGCCCCTGT          CCTCCCGACC          TCCATGCCCA          CTCGGGGGCA          TGCTGGGGAT          GCGGTGGGCT
CGCGGGGACA          GGAGGGCTGG          AGGTACGGGT          GAGCCCCCGT          ACGACCCCTA          CGCCACCCGA

2170                2180                2190                2200                2210                2220
CTATGGCTTC          TGAGGCGGAA          AGAACCAGCT          GGGGCTCTAG          GGGGTATCCC          CACGCGCCCT
GATACCGAAG          ACTCCGCCTT          TCTTGGTCGA          CCCCGAGATC          CCCCATAGGG          GTGCGCGGGA

2230                2240                2250                2260                2270                2280
GTAGCGGCGC          ATTAAGCGCG          GCGGGTGTGG          TGGTTACGCG          CAGCGTGACC          GCTACACTTG
CATCGCCGCG          TAATTCGCGC          CGCCCACACC          ACCAATGCGC          GTCGCACTGG          CGATGTGAAC

2290                2300                2310                2320                2330                2340
CCAGCGCCCT          AGCGCCCGCT          CCTTTCGCTT          TCTTCCCTTC          CTTTCTCGCC          ACGTTCGCCG
GGTCGCGGGA          TCGCGGGCGA          GGAAAGCGAA          AGAAGGGAAG          GAAAGAGCGG          TGCAAGCGGC

2350                2360                2370                2380                2390                2400
GCTTTCCCCG          TCAAGCTCTA          AATCGGGGCA          TCCCTTTAGG          GTTCCGATTT          AGTGCTTTAC
CGAAAGGGGC          AGTTCGAGAT          TTAGCCCCGT          AGGGAAATCC          CAAGGCTAAA          TCACGAAATG
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FIG. 19E
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

2410	2420	2430	2440	2450	2460
GGCACCTCGA	CCCCAAAAAA	CTTGATTAGG	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT
CCGTGGAGCT	GGGGTTTTTT	GAACTAATCC	CACTACCAAG	TGCATCACCC	GGTAGCGGGA
2470	2480	2490	2500	2510	2520
GATAGACGGT	TTTTCGCCCT	TTGACGTTGG	AGTCCACGTT	CTTTAATAGT	GGACTCTTGT
CTATCTGCCA	AAAAGCGGGA	AACTGCAACC	TCAGGTGCAA	GAAATTATCA	CCTGAGAACA
2530	2540	2550	2560	2570	2580
TCCAAACTGG	AACAACACTC	AACCCTATCT	CGGTCTATTC	TTTTGATTTA	TAAGGGATTT
AGGTTTGACC	TTGTTGTGAG	TTGGGATAGA	GCCAGATAAG	AAAACTAAAT	ATTCCCTAAA
2590	2600	2610	2620	2630	2640
TGGGGATTTC	GGCCTATTGG	TTAAAAAATG	AGCTGATTTA	ACAAAAATTT	AACGCGAATT
ACCCCTAAAG	CCGGATAACC	AATTTTTTAC	TCGACTAAAT	TGTTTTTAAA	TTGCGCTTAA
2650	2660	2670	2680	2690	2700
AATTCTGTGG	AATGTGTGTC	AGTTAGGGTG	TGGAAAGTCC	CCAGGCTCCC	CAGGCAGGCA
TTAAGACACC	TTACACACAG	TCAATCCCAC	ACCTTTCAGG	GGTCCGAGGG	GTCCGTCCGT
2710	2720	2730	2740	2750	2760
GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	CTAACTCCGC
CTTCATACGT	TTCGTACGTA	GAGTTAATCA	GTCGTTGGTA	TCAGGGCGGG	GATTGAGGCG
2770	2780	2790	2800	2810	2820
CCATCCCGCC	CCTAACTCCG	CCCAGTTCCG	CCCATTCTCC	GCCCCATGGC	TGACTAATTT
GGTAGGGCGG	GGATTGAGGC	GGGTCAAGGC	GGGTAAGAGG	CGGGGTACCG	ACTGATTAAA
2830	2840	2850	2860	2870	2880
TTTTTATTTA	TGCAGAGGCC	GAGGCCGCCT	CGGCCTCTGA	GCTATTCCAG	AAGTAGTGAG
AAAAATAAAT	ACGTCTCCGG	CTCCGGCGGA	GCCGGAGACT	CGATAAGGTC	TTCATCACTC
2890	2900	2910	2920	2930	2940
GAGGCTTTTT	TGGAGGCCTA	GGCTTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGCGATTT
CTCCGAAAAA	ACCTCCGGAT	CCGAAAACGT	TTTTCGAACC	TGTCGAGTCC	CGACGCTAAA
2950	2960	2970	2980	2990	3000
CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	CCCGCTGCCA
GCGCGGTTTG	AACTGCCGTT	AGGATCGCAC	TTCCGACCAT	CCTAAAATAG	GGGCGACGGT

FIG. 19F
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

FIG. 19G
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

FIG. 19H
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

4210
CTTTTTAATT
GAAAAATTAA

4220
TGTAAAGGGG
ACATTTCCCC

4230
TTAATAAGGA
AATTATTCCT

4240
ATATTTGATG
TATAAACTAC

4250
TATAGTGCCT
ATATCACGGA

4260
TGACTAGAGA
ACTGATCTCT

4270
TCATAATCAG
AGTATTAGTC

4280
CCATACCACA
GGTATGGTGT

4290
TTTGTAGAGG
AAACATCTCC

4300
TTTTACTTGC
AAAATGAACG

4310
TTTAAAAAAC
AAATTTTTTG

4320
CTCCCACACC
GAGGGTGTGG

4330
TCCCCCTGAA
AGGGGGACTT

4340
CCTGAAACAT
GGACTTTGTA

4350
AAAATGAATG
TTTTACTTAC

4360
CATTGTTGT
GTTAACAACA

4370
TGTTAACTTG
ACAATTGAAC

4380
TTTATTGCAG
AAATAACGTC

4390
CTTATAATGG
GAATATTACC

4400
TTACAAATAA
AATGTTTATT

4410
AGCAATAGCA
TCGTTATCGT

4420
TCACAAATTT
AGTGTTTAAA

4430
CACAAATAAA
GTGTTTATTT

4440
GCATTTTTTT
CGTAAAAAAA

4450
CACTGCATTC
GTGACGTAAG

4460
TAGTTGTGGT
ATCAACACCA

4470
TTGTCCAAAC
AACAGGTTTG

4480
TCATCAATGT
AGTAGTTACA

4490
ATCTTATCAT
TAGAATAGTA

4500
GTCTGGATCG
CAGACCTAGC

4510
GCTGGATGAT
CGACCTACTA

4520
CCTCCAGCGC
GGAGGTCGCG

4530
GGGGATCTCA
CCCCTAGAGT

4540
TGCTGGAGTT
ACGACCTCAA

4550
CTTCGCCCAC
GAAGCGGGTG

4560
CCCAACTTGT
GGGTTGAACA

4570
TTATTGCAGC
AATAACGTCG

4580
TTATAATGGT
AATATTACCA

4590
TACAAATAAA
ATGTTTATTT

4600
GCAATAGCAT
CGTTATCGTA

4610
CACAAATTTC
GTGTTTAAAG

4620
ACAAATAAAG
TGTTTATTTC

4630
CATTTTTTTC
GTAAAAAAAG

4640
ACTGCATTCT
TGACGTAAGA

4650
AGTTGTGGTT
TCAACACCAA

4660
TGTCCAAACT
ACAGGTTTGA

4670
CATCAATGTA
GTAGTTACAT

4680
TCTTATCATG
AGAATAGTAC

4690
TCTGTATACC
AGACATATGG

4700
GTCGACCTCT
CAGCTGGAGA

4710
AGCTAGAGCT
TCGATCTCGA

4720
TGGCGTAATC
ACCGCATTAG

4730
ATGGTCATAG
TACCAGTATC

4740
CTGTTTCCTG
GACAAAGGAC

4750
TGTGAAATTG
ACACTTTAAC

4760
TTATCCGCTC
AATAGGCGAG

4770
ACAATTCCAC
TGTTAAGGTG

4780
ACAACATACG
TGTTGTATGC

4790
AGCCGGAAGC
TCGGCCTTCG

4800
ATAAAGTGTA
TATTTCACAT

FIG. 19I
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

```
4810
AAGCCTGGGG
TTCGGACCCC

4820
TGCCTAATGA
ACGGATTACT

4830
GTGAGCTAAC
CACTCGATTG

4840
TCACATTAAT
AGTGTAATTA

4850
TGCGTTGCGC
ACGCAACGCG

4860
TCACTGCCCG
AGTGACGGGC

4870
CTTTCCAGTC
GAAAGGTCAG

4880
GGGAAACCTG
CCCTTTGGAC

4890
TCGTGCCAGC
AGCACGGTCG

4900
TGCATTAATG
ACGTAATTAC

4910
AATCGGCCAA
TTAGCCGGTT

4920
CGCGCGGGGA
GCGCGCCCCT

4930
GAGGCGGTTT
CTCCGCCAAA

4940
GCGTATTGGG
CGCATAACCC

4950
CGCTCTTCCG
GCGAGAAGGC

4960
CTTCCTCGCT
GAAGGAGCGA

4970
CACTGACTCG
GTGACTGAGC

4980
CTGCGCTCGG
GACGCGAGCC

5050
AATCAGGGGA
TTAGTCCCCT

5060
TAACGCAGGA
ATTGCGTCCT

5070
AAGAACATGT
TTCTTGTACA

5080
GAGCAAAAGG
CTCGTTTTCC

5090
CCAGCAAAAG
GGTCGTTTTC

5100
GCCAGGAACC
CGGTCCTTGG

5110
GTAAAAAGGC
CATTTTTCCG

5120
CGCGTTGCTG
GCGCAACGAC

5130
GCGTTTTTCC
CGCAAAAAGG

5140
ATAGGCTCCG
TATCCGAGGC

5150
CCCCCCTGAC
GGGGGGACTG

5160
GAGCATCACA
CTCGTAGTGT

5170
AAAATCGACG
TTTTAGCTGC

5180
CTCAAGTCAG
GAGTTCAGTC

5190
AGGTGGCGAA
TCCACCGCTT

5200
ACCCGACAGG
TGGGCTGTCC

5210
ACTATAAAGA
TGATATTTCT

5220
TACCAGGCGT
ATGGTCCGCA

5230
TTCCCCCTGG
AAGGGGGACC

5240
AAGCTCCCTC
TTCGAGGGAG

5250
GTGCGCTCTC
CACGCGAGAG

5260
CTGTTCCGAC
GACAAGGCTG

5270
CCTGCCGCTT
GGACGGCGAA

5280
ACCGGATACC
TGGCCTATGG

5290
TGTCCGCCTT
ACAGGCGGAA

5300
TCTCCCTTCG
AGAGGGAAGC

5310
GGAAGCGTGG
CCTTCGCACC

5320
CGCTTTCTCA
GCGAAAGAGT

5330
ATGCTCACGC
TACGAGTGCG

5340
TGTAGGTATC
ACATCCATAG

5350
TCAGTTCGGT
AGTCAAGCCA

5360
GTAGGTCGTT
CATCCAGCAA

5370
CGCTCCAAGC
GCGAGGTTCG

5380
TGGGCTGTGT
ACCCGACACA

5390
GCACGAACCC
CGTGCTTGGG

5400
CCCGTTCAGC
GGGCAAGTCG
```

FIG. 19J
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

FIG. 19K
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

FIG. 19L
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

6610 6620 6630 6640 6650 6660
GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGTAGA AAATGAAAGT

6670 6680 6690 6700 6710 6720
CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG
GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTACG GCGTTTTTTC CCTTATTCCC

6730 6740 6750 6760 6770 6780
CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTTATC
GCTGTGCCTT TACAACTTAT GAGTATGAGA AGGAAAAAGT TATAATAACT TCGTAAATAG

6790 6800 6810 6820 6830 6840
AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

6850 6860 6870 6880 6890 6900
GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CGACGGATCG GGAGATCTGC
CCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA GCTGCCTAGC CCTCTAGACG

6910 6920 6930 6940 6950 6960
TAGGTGACCT GAGGCGCGCC GGCTTCGAAT AGCCAGAGTA ACCTTTTTTT TTAATTTTAT
ATCCACTGGA CTCCGCGCGG CCGAAGCTTA TCGGTCTCAT TGGAAAAAAA AATTAAAATA

6970 6980 6990 7000 7010 7020
TTTATTTTAT TTTTGAGATG GAGTTTGGCG CCGATCTCCC GATCCCCTAT GGTCGACTCT
AAATAAAATA AAACTCTAC CTCAAACCGC GGCTAGAGGG CTAGGGGATA CCAGCTGAGA

7030 7040 7050 7060 7070 7080
CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
GTCATGTTAG ACGAGACTAC GGCGTATCAA TTCGGTCATA GACGAGGGAC GAACACAA

7090 7100 7110 7120 7130 7140
GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA
CCTCCAGCGA CTCATCACGC GCTCGTTTTA AATTCGATGT TGTTCCGTTC CGAACTGGCT

7150 7160 7170 7180 7190 7200
CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC
GTTAACGTAC TTCTTAGACG AATCCCAATC CGCAAAACGC GACGAAGCGC TACATGCCCG

FIG. 19M
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

7210 7220 7230 7240 7250 7260
CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC
GTCTATATGC GCAACTGTAA CTAATAACTG ATCAATTAAT ATCATTAGTT AATGCCCCAG

7270 7280 7290 7300 7310 7320
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC
TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG

7330 7340 7350 7360 7370 7380
TGACTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA

7390 7400 7410 7420 7430 7440
AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA
TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTG ATAAATGCCA TTTGACGGGT

7450 7460 7470 7480 7490 7500
CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

7510 7520 7530 7540 7550 7560
TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA
ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT

7570 7580 7590 7600 7610 7620
GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA
CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT

7630 7640 7650 7660 7670 7680
TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

7690 7700 7710 7720 7730 7740
TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TGTTGAGGCG

7750 7760 7770 7780 7790 7800
CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT
GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGA

FIG. 19N
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

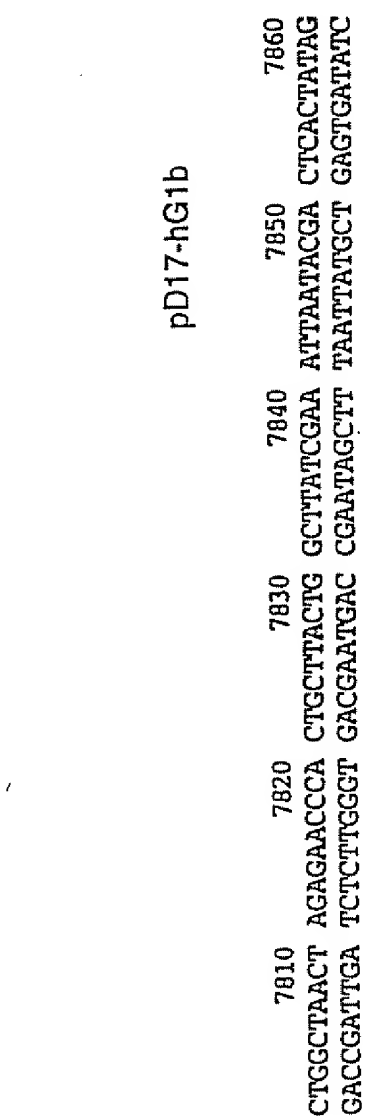

FIG. 20

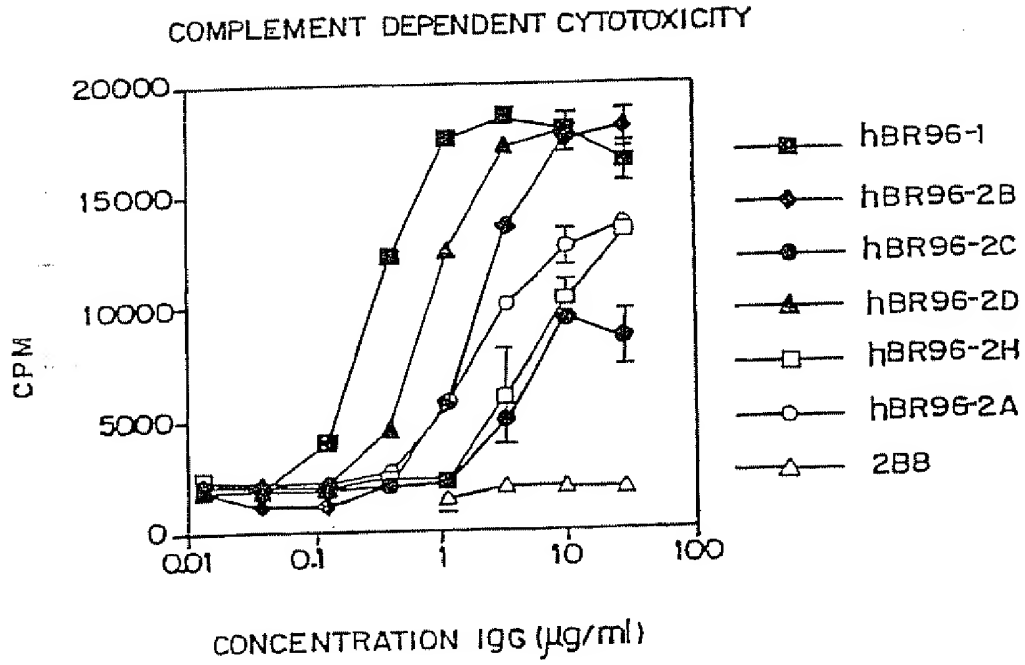
COMPLEMENT DEPENDENT CYTOTOXICITY
CPM
20000
15000
10000
5000
0
0.01
0.1
1
10
100
CONCENTRATION IgG (µg/ml)
hBR96-1
hBR96-2B
hBR96-2C
hBR96-2D
hBR96-2H
hBR96-2A
2B8

FIG. 21

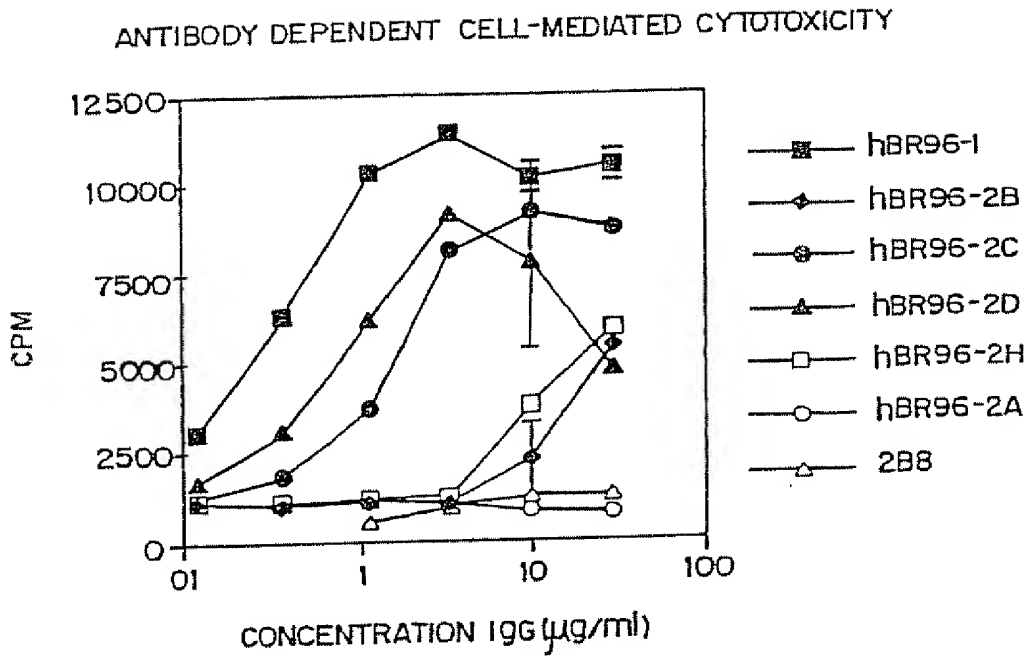
ANTIBODY DEPENDENT CELL-MEDIATED CYTOTOXICITY
12500
10000
7500
5000
2500
0
CPM
01
1
10
100
CONCENTRATION IgG (µg/ml)
hBR96-1
hBR96-2B
hBR96-2C
hBR96-2D
hBR96-2H
hBR96-2A
2B8

FIG.22

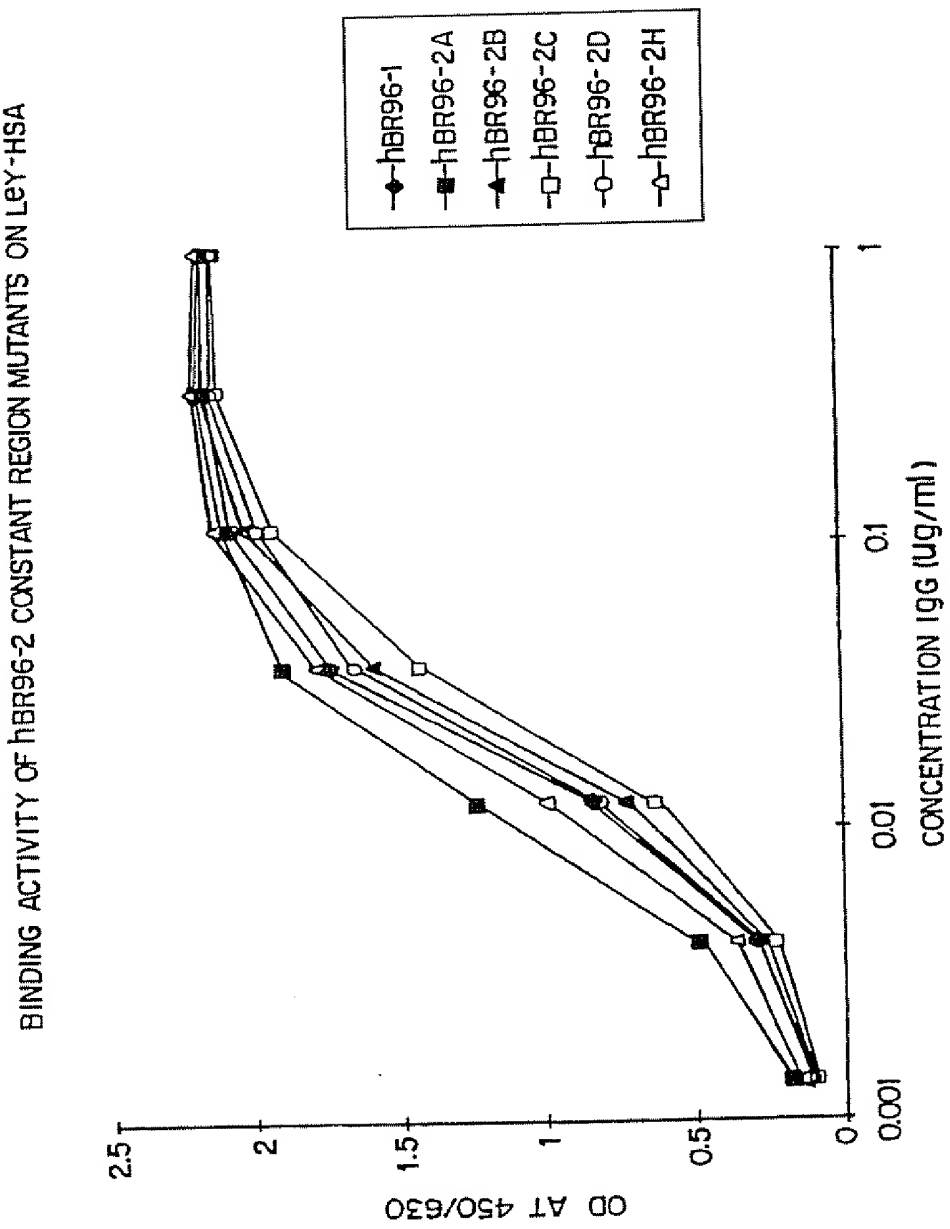
BINDING ACTIVITY OF hBR96-2 CONSTANT REGION MUTANTS ON LeY-HSA
hBR96-1
hBR96-2A
hBR96-2B
hBR96-2C
hBR96-2D
hBR96-2H
OD AT 450/630
2.5
2
1.5
1
0.5
0
0.001
0.01
0.1
1
CONCENTRATION IgG (ug/ml)

FIG.23

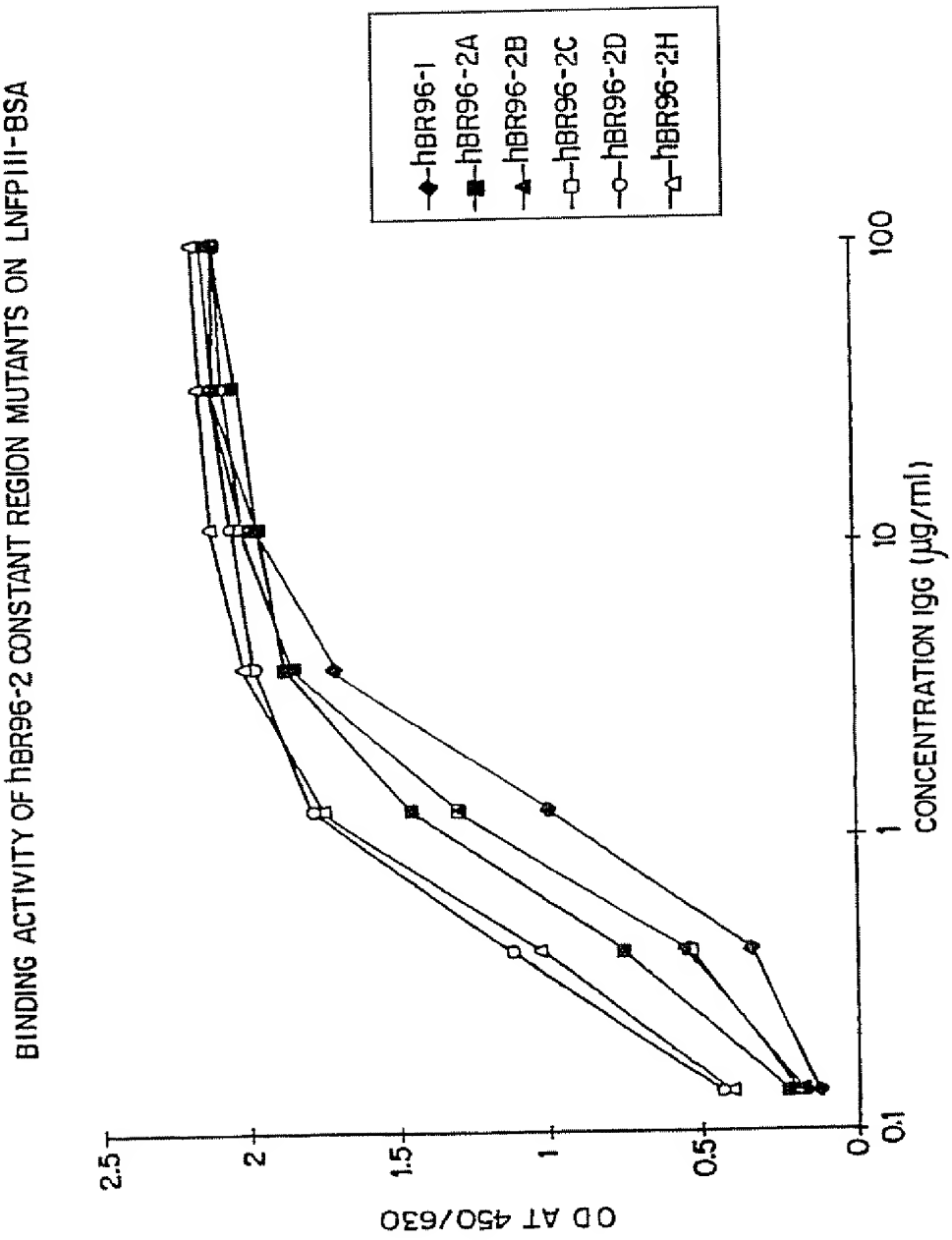
BINDING ACTIVITY OF hBR96-2 CONSTANT REGION MUTANTS ON LNFPIII-BSA
hBR96-I
hBR96-2A
hBR96-2B
hBR96-2C
hBR96-2D
hBR96-2H
OD AT 450/630
2.5
2
1.5
1
0.5
0
0.1
1
10
100
CONCENTRATION IgG (µg/ml)

FIG. 24A

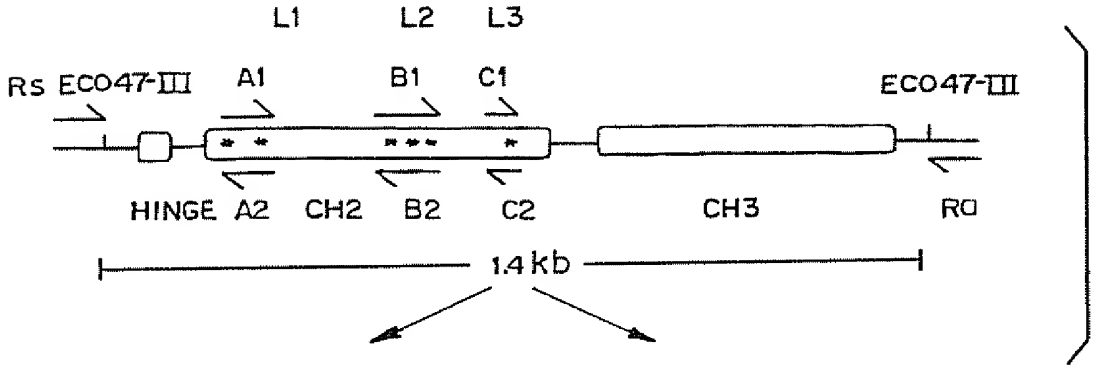

FIG. 24B

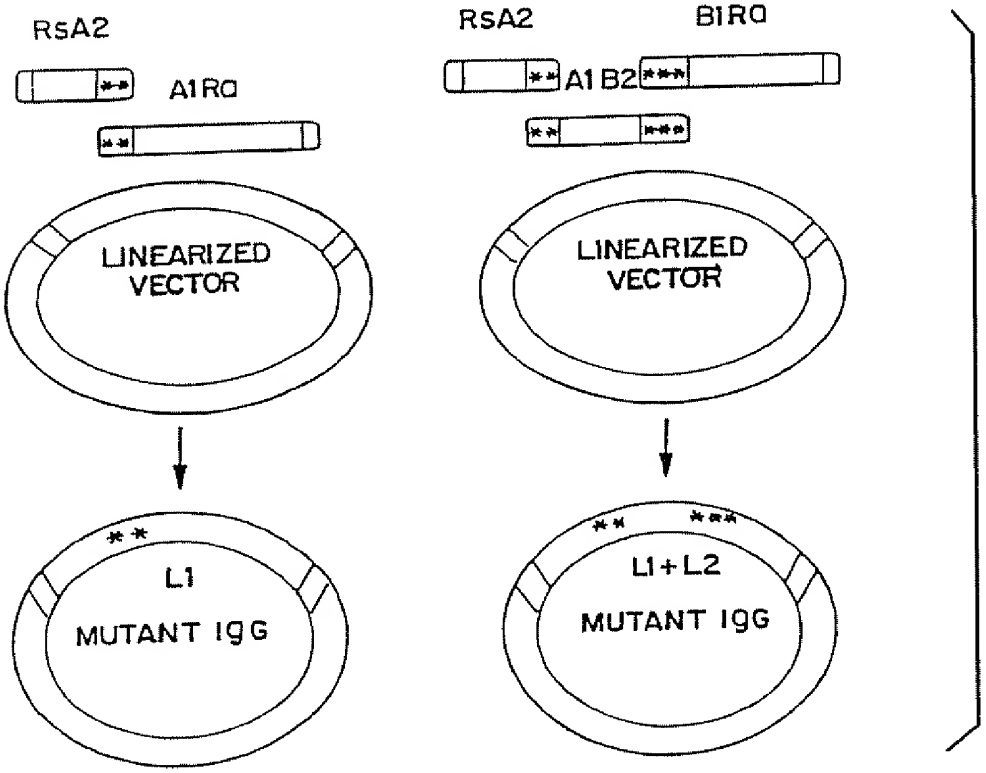

FIG.25

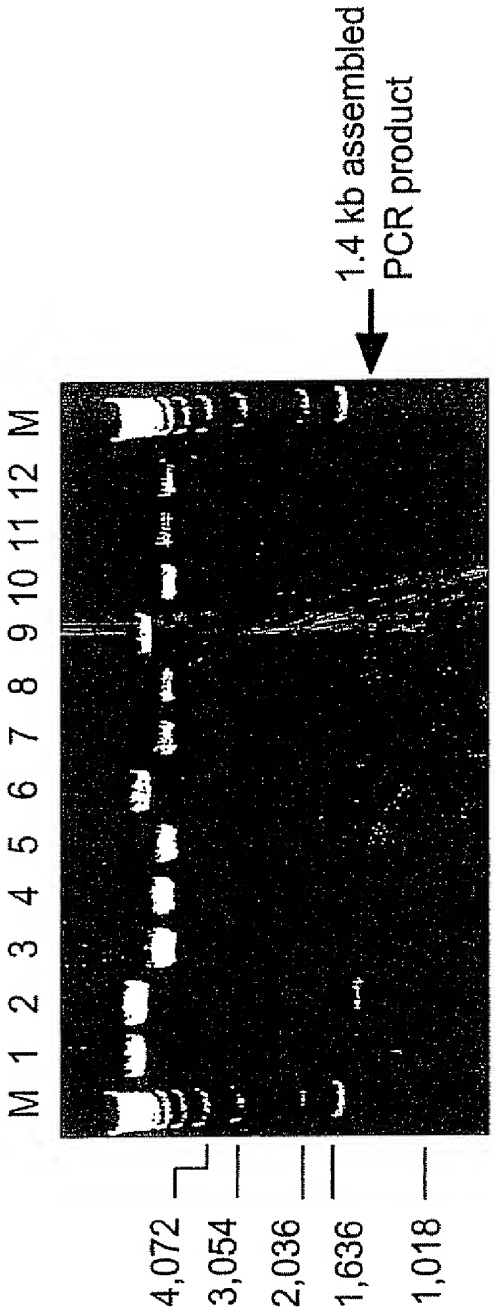
1.4 kb assembled
PCR product
M 1 2 3 4 5 6 7 8 9 10 11 12 M
4,072
3,054
2,036
1,636
1,018

FIG. 26

hBR96-2 Heavy Chain Variable Region (V_H)

(SEQ ID NO:24)

```
1               11              21              31              41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY

51          61              71              81              91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL

101             111
ADGAWFAYWG QGTLVTVSS
```

Human IgG1 Constant

(SEQ ID NO:25)

```
                        CH1
                       A STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
                                    CH2 235  237
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
                  318 320  322      331          CH3
TYRVVSVLTV LHQDWLNGKE YKDKVSNKAL PAPIEKTISK AKGQPREPQV

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

FIG. 27

hBR96-2A: Heavy Chain Variable Region (V_H)

(SEQ ID NO:24)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY

51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL

101 111
ADGAWFAYWG QGTLVTVSS

hBR96-2A: Human Heavy Chain IgG1 Constant Region ΔCH2

(SEQ ID NO:26)

A STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH

TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK

SCDKTHTCPP CP GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA

VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM

HEALHNHYTQ KSLSLSPGK

FIG. 28

(SEQ ID NO:27)

This sequence is the chi BR96 IgG1 with CH2 deleted.

VH

1 EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY

51 ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL

CH1

101 DDGAWFAYWG QGTLVTVSVA STKGPSVFPL APSSKSTSGG TAALGCLVKD

151 YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

CH3

201 ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPGQPREPQV YTLPPSRDEL

251 TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS

301 KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK